

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:29:15 ; Search time 40 Seconds
(without alignments)
767.445 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGWAVFLASRLGQGLL.....QNVDGLVLDLAVIRTLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1070241 seqs, 262374223 residues

Total number of hits satisfying chosen parameters: 1070241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	117	10	US-09-946-374-6
2	609	100.0	117	12	US-10-081-056-6
3	609	100.0	117	13	US-10-066-500-9
4	609	100.0	117	14	US-10-002-796-9
5	609	100.0	117	14	US-10-066-273-9
6	609	100.0	117	14	US-10-066-494-9
7	609	100.0	117	14	US-10-066-269-9
8	609	100.0	117	14	US-10-006-856A-6
9	609	100.0	117	14	US-10-066-211-9
10	609	100.0	117	14	US-10-066-193-9
11	609	100.0	117	14	US-10-006-818A-6
12	609	100.0	117	14	US-10-015-393A-6
13	609	100.0	117	14	US-10-015-869A-6
14	609	100.0	117	14	US-10-012-121A-6
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19	609	100.0	117	14	US-10-007-194A-6
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29	609	100.0	117	14	US-10-223-087-6
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37	609	100.0	117	14	US-10-223-089-6
38	609	100.0	117	14	US-10-017-407A-6
39	609	100.0	117	14	US-10-011-833A-6
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41	609	100.0	117	14	US-10-015-822A-6
42	609	100.0	117	14	US-10-015-387A-6
43	609	100.0	117	14	US-10-006-130A-6
44	609	100.0	117	14	US-10-006-172A-6
45	609	100.0	117	14	US-10-017-253A-6

ALIGNMENTS

RESULT 1

US-09-946-374-6

; Sequence 6, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Fan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

; FILE REFERENCE: P2830P1C1

; CURRENT APPLICATION NUMBER: US/09/946,374

; PRIOR FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
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; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-081-056-6
; Sequence 6, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081.056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522

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; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
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; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
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; PRIOR APPLICATION NUMBER: US 09/828,366
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; PRIOR APPLICATION NUMBER: US 09/854,208
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
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; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
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US-10-081-056-6

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Query Match      100.0%; Score 609; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSVDVTDQ 60

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Db 1 MIVFGWAVELASRQGGLLLTLESHIAHFLGTGGAATTMGNSCICRDDSDTDSVDFTQ 60
QY 61 QOAEASVPTATRSQPRDPVPRGRGPHPRKKNQVGLVDTLAVIRTLVDK 117
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RESULT 3
US-10-066-500-9
; Sequence 9, Application US/10066500
; Publication No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ahenkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
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; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
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; PRIOR APPLICATION NUMBER: 60/069694
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; PRIOR APPLICATION NUMBER: 60/169495
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; PRIOR APPLICATION NUMBER: 08/918874
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; PRIOR APPLICATION NUMBER: 09/202088
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 09/254311
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/254460
; PRIOR FILING DATE: 1999-03-09
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; PRIOR FILING DATE: 1999-03-05
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; PRIOR APPLICATION NUMBER: 09/380137

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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 13; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVEGNAVFLASRLGGGLLTLEEHIAHFLGTGGAATTWNSCICRDSGTDSDVDTQQ 60
Db 1 MIVEGNAVFLASRLGGGLLTLEEHIAHFLGTGGAATTWNSCICRDSGTDSDVDTQQ 60

Qy 61 QOAENSAVPTADTRSQDRDPVPRPRRGSGPHEPRRKQKQNDGLVLDTLAVIRTLVDK 117
Db 61 QOAENSAVPTADTRSQDRDPVPRPRRGSGPHEPRRKQKQNDGLVLDTLAVIRTLVDK 117

RESULT 4
US-10-002-796-9
; Sequence 9, Application US/10002796
; Publication No. US2003032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Deenoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watarabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C1
; CURRENT APPLICATION NUMBER: US/10/002.796
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 61 QQAENSAVPTADTRSQRPDPVPRPRGRGPHPRKQNVGDLVLTFLAVITLVDK 117

RESULT 5

US-10-066-273-9

Sequence 9, Application US/10066273

Publication No. US20030032062A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi

APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein

APPLICANT: Luc Desnoyers

APPLICANT: Dan L. Eaton

APPLICANT: Napoleone Ferrara

APPLICANT: Sherman Fong

APPLICANT: Wei-Qiang Gao

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APPLICANT: Mary E. Gerritsen

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APPLICANT: Paul J. Godowski

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APPLICANT: Jennie P. Macher

APPLICANT: Mary A. Napier

APPLICANT: James Pan

APPLICANT: Nicholas F. Paoni

APPLICANT: Margaret Ann Roy

APPLICANT: Timothy A. Stewart

APPLICANT: Daniel Tumas

APPLICANT: Colin K. Watanabe

APPLICANT: P. Mickey Williams

APPLICANT: William I. Wood

APPLICANT: Zemin Zang

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

FILE REFERENCE: P3130R1C2

CURRENT APPLICATION NUMBER: US/10/066,273

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 10/002,796

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/056974

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Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGNAVLASLSGGLLLTLEEHIAHPLGTGGAAATMGNSICRDDSGTDDSDVDTQQ 60
 Db 1 MIVFGNAVLASLSGGLLLTLEEHIAHPLGTGGAAATMGNSICRDDSGTDDSDVDTQQ 60
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 Db 61 QQAENSAPVTADTRSPDPVPPRGRGPHPRKKQNVGGLVDTLAVITLVDK 117

RESULT 6

US-10-066-494-9
 ; Sequence 9, Application US/10066494
 ; Publication No. US20030032063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi
 ; APPLICANT: Kevin P. Baker
 ; APPLICANT: David A. Botstein
 ; APPLICANT: Luc Desnoyers
 ; APPLICANT: Dan L. Eaton
 ; APPLICANT: Napoleone Ferrara
 ; APPLICANT: Sherman Fong
 ; APPLICANT: Wei-Qiang Gao
 ; APPLICANT: Hanspeter Gerber
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 ; APPLICANT: Daniel Tumas
 ; APPLICANT: Colin K. Watanabe
 ; APPLICANT: P. Mickey Williams
 ; APPLICANT: William I. Wood
 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3130R1C9
 ; CURRENT APPLICATION NUMBER: US/10/066,494
 ; CURRENT FILING DATE: 2002-02-01
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 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVTQQ 60
 DB 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVTQQ 60
 QY 61 QQAENSAVPTADTRSQPRDPVPPRRGRGPHEPRRKKQNVGLVLDLTAIVITLVDK 117
 DB 61 QQAENSAVPTADTRSQPRDPVPPRRGRGPHEPRRKKQNVGLVLDLTAIVITLVDK 117

RESULT 7
 US-10-066-269-9
 ; Sequence 9, Application US/10066269
 ; Publication NO. US2003004014A1

GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerlitsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
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APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C4
CURRENT APPLICATION NUMBER: US/10/066,269
CURRENT FILING DATE: 2002-02-01
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;; PRIOR APPLICATION NUMBER: PCT/US99/21090
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;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGGLLTLEEHIAHFLGTGGAATTGNSCICRDSGTDSDVDVTDQ 60
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Db 1 MIVFGWAVFLASRLGGLLTLEEHIAHFLGTGGAATTGNSCICRDSGTDSDVDVTDQ 60
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QY 61 QOENSAPVPTADTSQPRDPVPRRGPGPHEPRRKQNVGDLVLDTLAVIRTLVDK 117
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Db 61 QOENSAPVPTADTSQPRDPVPRRGPGPHEPRRKQNVGDLVLDTLAVIRTLVDK 117
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RESULT 8
US-10-006-856A-6
; Sequence 6, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2830P1C14
;; CURRENT APPLICATION NUMBER: US/10/006,856A
;; CURRENT FILING DATE: 2002-05-10
;; NUMBER OF SEQ ID NOS: 477
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 6
;; LENGTH: 117
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 1-16
;; OTHER INFORMATION: Signal Peptide
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 18-21, 32-38, 34-40, 35-41, 51-57
;; OTHER INFORMATION: N-Myristoylation Site.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 22-26, 50-54, 113-117
;; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-856A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QOENSAPVPTADTSQPRDPVPRRGPGPHEPRRKQNVGDLVLDTLAVIRTLVDK 117
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Db 61 QOENSAPVPTADTSQPRDPVPRRGPGPHEPRRKQNVGDLVLDTLAVIRTLVDK 117
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RESULT 9
US-10-066-211-9
; Sequence 9, Application US/10066211
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
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APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C8
CURRENT APPLICATION NUMBER: US/10/066,211
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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PRIOR APPLICATION NUMBER: 09/380139
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PRIOR APPLICATION NUMBER: 09/403296
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PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
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PRIOR APPLICATION NUMBER: 09/423844
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 09/522342
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/548815
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/866028
PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 09/870574
 ; PRIOR FILING DATE: 2001-05-30
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 ; PRIOR APPLICATION NUMBER: PCT/US99/05028
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/20111
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 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MIVFGWAVFLASRLGQLLLTLEEHIAHFLGTGGAATTWNSICRDDSGLTDSVDTQ 60
 Db 1 MIVFGWAVFLASRLGQLLLTLEEHIAHFLGTGGAATTWNSICRDDSGLTDSVDTQ 60
 Qy 61 QOENSAPVPTADTSQRPDPVRRGRGPHPEPRKKQNDGLVLDLTLAVIRTLVDK 117
 Db 61 QOENSAPVPTADTSQRPDPVRRGRGPHPEPRKKQNDGLVLDLTLAVIRTLVDK 117

RESULT 10
 US-10-066-193-9

; Sequence 9, Application US/10066193
 ; Publication No. US2003004902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi
 ; APPLICANT: Kevin P. Baker
 ; APPLICANT: David A. Botstein
 ; APPLICANT: Luc Desnoyers
 ; APPLICANT: Dan L. Eaton
 ; APPLICANT: Napoleone Ferrara
 ; APPLICANT: Sherman Fong
 ; APPLICANT: Wei-Qiang Gao
 ; APPLICANT: Hanspeter Gerber
 ; APPLICANT: Mary E. Gerritsen
 ; APPLICANT: Audrey Goddard
 ; APPLICANT: Paul J. Godowski
 ; APPLICANT: Austin L. Gurney
 ; APPLICANT: Ivar J. Kjavlin
 ; APPLICANT: Jennie P. Mather
 ; APPLICANT: Mary A. Napier
 ; APPLICANT: James Pan
 ; APPLICANT: Nicholas F. Paoni
 ; APPLICANT: Margaret Ann Roy
 ; APPLICANT: Timothy A. Stewart
 ; APPLICANT: Daniel Tumas

; APPLICANT: Colin K. Watanabe
 ; APPLICANT: P. Mickey Williams
 ; APPLICANT: William I. Wood
 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3130R1C3
 ; CURRENT APPLICATION NUMBER: US/10/066,193
 ; CURRENT FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: 10/002,796
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 09/808689
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/870574
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; PRIOR FILING DATE: 2001-06-01
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; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: PCT/US98/14552
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; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDSGTDSDVDTOQ 60
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDSGTDSDVDTOQ 60
Qy 61 QQAENSAVPTADTRSPQRPVPRPRGRGPHEPRRKQNVGVLVLTAVIRTLVOK 117
Db 61 QQAENSAVPTADTRSPQRPVPRPRGRGPHEPRRKQNVGVLVLTAVIRTLVOK 117

RESULT 11

US-10-006-818A-6
; Sequence 6, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT

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/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 1-16
/ OTHER INFORMATION: Signal Peptide
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
/ OTHER INFORMATION: N-Myristoylation Site.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 22-26, 50-54, 113-117
/ OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-818A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60

Qy      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117
Db      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117

RESULT 12
US-10-015-393A-6
; Sequence 6, Application US/10015393A
; Publication NO. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-393A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60

Qy      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117
Db      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117

RESULT 13
US-10-015-869A-6
; Sequence 6, Application US/10015869A
; Publication NO. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-869A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDSVDTQQ 60

Qy      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117
Db      61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLVDK 117

RESULT 14
US-10-012-121A-6
; Sequence 6, Application US/10012121A
; Publication NO. US20030073810A1
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DB	1	MIVFGWAVFLASRLGQGLLLTLEBHIAFLTGGAATMGNSICRRDSDTDSVDTQ	60												
QY	61	QQAENSAVPTATRSQPDVPPRRGRGPHPRKKQVGLVLDLTLAVIRTLVDK	117												
DB	61	QQAENSAVPTATRSQPDVPPRRGRGPHPRKKQVGLVLDLTLAVIRTLVDK	117												
RESULT 15															
US-10-006-116A-6															
Sequence 6, Application US/10006116A															
Publication No. US20030082626A1															
GENERAL INFORMATION:															
APPLICANT: Baker, Kevin P.															
APPLICANT: Botstein, David															
APPLICANT: Desnovers, Luc															
APPLICANT: Eaton, Dan I.															
APPLICANT: Ferrara, Napoleone															
APPLICANT: Fong, Sherman															
APPLICANT: Goddard, Audrey															
APPLICANT: Godowski, Paul J.															
APPLICANT: Grimaldi, Christopher J.															
APPLICANT: Gurney, Austin L.															
APPLICANT: Hillan, Kenneth J.															
APPLICANT: Pan, James															
APPLICANT: Paoni, Nicholas F.															
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic															
TITLE OF INVENTION: Acids Encoding the Same															
FILE REFERENCE: P2830PIC20															
CURRENT FILING DATE: 2001-12-07															
Prior Application removed - See File Wrapper or Palm															
NUMBER OF SEQ ID NOS: 477															
SEQ ID NO 6															
LENGTH: 117															
TYPE: PRT															
ORGANISM: Homo sapiens															
NAME/KEY: sig_peptide															
LOCATION: 1-16															
OTHER INFORMATION: Signal Peptide															
FEATURE:															
NAME/KEY: misc_feature															
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57															
OTHER INFORMATION: N-Myristoylation Site.															
FEATURE:															
NAME/KEY: misc_feature															
LOCATION: 22-26, 50-54, 113-117															
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.															
US-10-012-121A-6															
Query Match 100.0%; Score 609; DB 14; Length 117;															
Best Local Similarity 100.0%; Pred. No. 1.7e-58;															
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;															

; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
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; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 609; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-58;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRSIGQGLLLTLESHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVDIQQ 60

Db 1 MIVFGWAVFLASRSIGQGLLLTLESHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVDIQQ 60

QY 61 QQAENSAPVTADTRSQPRDPVPPRGRGPPEPRKKQNVLDGLVLDTLAVIRTLVDK 117

Db 61 QQAENSAPVTADTRSQPRDPVPPRGRGPPEPRKKQNVLDGLVLDTLAVIRTLVDK 117

Search completed: April 2, 2004, 10:32:34

Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 10:28:10 ; Search time 22 Seconds
(without alignments)
274.556 Million cell updates/sec

Title: US-10-002-796-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRLQGLL.....QNVGILVDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	13.1	460	4	US-09-252-991A-20180
2	79	13.0	287	4	US-09-252-991A-30267
3	78	12.8	1527	4	US-09-418-710-27
4	78	12.8	1531	4	US-09-418-710-29
5	75	12.3	433	2	US-08-466-120-2
6	75	12.3	433	5	PCT-US94-07266-2
7	75	12.3	1525	4	US-09-418-710-69
8	74.5	12.2	462	2	US-08-865-597A-2
9	73.5	12.1	2509	2	US-08-149-097D-35
10	73	12.0	623	3	US-09-029-348-3
11	73	12.0	626	3	US-09-029-348-2
12	72.5	11.9	333	4	US-09-252-991A-28443
13	71.5	11.7	562	4	US-09-252-991A-20178
14	71.5	11.7	566	4	US-09-252-991A-18531
15	71	11.7	863	4	US-09-252-991A-26099
16	70	11.5	386	4	US-09-252-991A-32927
17	69	11.3	191	2	US-08-390-665A-198
18	69	11.3	191	2	US-08-390-665A-199
19	69	11.3	191	2	US-08-390-665A-200
20	69	11.3	191	2	US-08-390-665A-201
21	69	11.3	191	2	US-08-390-665A-202
22	69	11.3	191	2	US-08-390-665A-203
23	69	11.3	191	5	PCT-US95-10398-198
24	69	11.3	191	5	PCT-US95-10398-199
25	69	11.3	191	5	PCT-US95-10398-200
26	69	11.3	191	5	PCT-US95-10398-201
27	69	11.3	191	5	PCT-US95-10398-202

28	69	11.3	191	5	PCT-US95-10398-203
29	69	11.3	319	4	US-08-635-886C-226
30	69	11.3	319	4	US-08-974-690C-226
31	69	11.3	350	4	US-09-252-991A-19537
32	69	11.3	498	4	US-09-354-151-2
33	69	11.3	778	4	US-09-198-452A-508
34	69.5	11.2	788	2	US-08-918-914-4
35	68	11.2	149	4	US-09-252-991A-21599
36	68	11.2	379	4	US-09-252-991A-31693
37	68	11.2	882	3	US-09-413-814-78
38	67.5	11.1	518	4	US-09-252-991A-18753
39	67.5	11.1	727	2	US-08-475-844-9
40	67.5	11.1	727	5	PCT-US95-08429-9
41	67.5	11.1	1298	2	US-08-650-473-2
42	67.5	11.1	1298	3	US-09-259-821A-2
43	67.5	11.1	1298	3	US-08-843-659-2
44	67	11.0	393	4	US-09-432-470-2
45	67	11.0	393	4	US-09-432-470-4

ALIGNMENTS

RESULT 1
US-09-252-991A-20180
; Sequence 20180, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20180
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20180

Query Match	13.1%	Score 80;	DB 4;	Length 460;
Best Local Similarity	28.6%	Pred. No. 0.42;		
Matches	20;	Conservative	11;	Mismatches 23; Indels 16; Gaps 2;
QY	32	GTGGAATTMGNSICRDSGTDDSDVTCQQAENSAVETADTRSQPRDPVPPRRGRGPH	91	
Db	373	CGGQAQVQAG-----EQADPEQRRVPGEAQIA-----NRGDDPVPPGERRGDH	416	
QY	92	EPRKKQNV	101	
Db	417	EQQRQGRHVD	426	

RESULT 2
US-09-252-991A-30267
; Sequence 30267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30267
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30267

Query Match      13.0%; Score 79; DB 4; Length 287;
Best Local Similarity 37.5%; Pred. No. 0.3;
Matches 21; Conservative 7; Mismatches 24; Indels 4; Gaps 1;

QY 51 GTDSDVDTQCOQAENS AVPTADTRSQRPDPVRP-----RRGRGPHPRKKQNVG 102
Db 15 GDDGPKRTQRRRDHPAGVAVARPGARPRRRPGGLAGRGCGAGKRRRRRQVPG 70

RESULT 3
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match      12.8%; Score 78; DB 4; Length 1527;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDSVDTQCOQAENS AVPTADTRSQRPDPVR-----PP-----RRGRGPHPR 95
Db 1255 EDESEDEEEEEEEDYEVAGLRLPRKTIKRGHSVIPPAARSGRRPGKPKHSTR 1314

QY 96 KK-----QNVDTGLVLD 107
Db 1315 SQKAPPVDDAEVDVLT 1334

RESULT 4
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match      12.8%; Score 78; DB 4; Length 1531;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDSVDTQCOQAENS AVPTADTRSQRPDPVR-----PP-----RRGRGPHPR 95
Db 1259 EDESEDEEEEEEEDYEVAGLRLPRKTIKRGHSVIPPAARSGRRPGKPKHSTR 1318

QY 96 KK-----QNVDTGLVLD 107
Db 1319 SQKAPPVDDAEVDVLT 1338

RESULT 5
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5863284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07366
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

Query Match      12.3%; Score 75; DB 2; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3;

QY 35 GAATTGNSCTCRDSDSDVDTQCOQAENS AVPTA-DTRSQ-PRDP--VRPGRGPR 90
Db 29 GSOAQGGSCILREARNPHSAGGTAGVGLAAEATLTLTRAEPPSEPTFIRPKKGP 88

RESULT 6
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266
```

GENERAL INFORMATION:
APPLICANT: CAO, ET AL.
TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07366
FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-07266-2

Query Match 12.3%; Score 75; DB 5; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5; Indels 23; Gaps 3;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3;
QY 35 GAATTGMSICRDSGTDSDVDTQQQAENSAPVTA-DTRSQ-PRDP--VRPPRRGRGP 90
Db 29 GSAQGGSSCILREARMPHSAGTAGVGLAAEPTALLTRAEPPEPTAIRPKKKGK 88

RESULT 7
US-09-418-710-69
Sequence 69, Application US/09418710
Patent No. 6596482
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 69
LENGTH: 1525
TYPE: PRT
ORGANISM: Homo sapiens
US-09-418-710-69

Query Match 12.3%; Score 75; DB 4; Length 1525;
Best Local Similarity 27.9%; Pred. No. 7.9;
Matches 24; Conservative 12; Mismatches 24; Indels 26; Gaps 4;
QY 48 DDSGTDDSDV-----TQQQAENSAPVTAATRSQPRDPVR-----PP-----RRGR 88
Db 1246 EESASESDESDSEEEEEEEDYEVAGLRPRKTIKRGKHSVIPPAARSGRRPGK 1305
QY 89 GPHEPRRK-----QNVDLGLVLT 107
Db 1306 KPHSTRSQPKAPPVDAEVDLVLQT 1331

RESULT 8
US-08-865-597A-2
Sequence 2, Application US/08865597A
Patent No. 5973131
GENERAL INFORMATION:
APPLICANT: Cao, Liang
APPLICANT: Yuen, Kwok Yung
TITLE OF INVENTION: PENNICILLUM MARNEFFEI ANTIGENIC PROTEIN 1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,597A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 50288-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-865-597A-2

Query Match 12.2%; Score 74.5; DB 2; Length 462;
Best Local Similarity 25.2%; Pred. No. 1.9; Indels 36; Gaps 1;
Matches 21; Conservative 10; Mismatches 36; Indels 5; Gaps 1;
QY 12 SRSLGQGLLLTLEBHIAHFLGTGGAATMGNSCICRDSGTDSDVDTQQQAENSAPVTA 71
Db 328 SRQLSDGIAAGIKKGIDAFAGTGPAPTTST-----PEASTAPAPSTPPPTEDTLVPAT 382
QY 72 DTRSQPRDPVP 83
Db 383 STPAPGPAPTAP 394

RESULT 9
US-08-149-097D-35
Sequence 35, Application US/08149097D
Patent No. 5874236
GENERAL INFORMATION:
APPLICANT: Harpold, Michael

OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-2

Query Match 12.0%; Score 73; DB 3; Length 626;
Best Local Similarity 28.8%; Pred. No. 4.2; Indels 28; Gaps 7;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;
QY 16 GQGLLLTLEH---IAHFLGTGGAATTMGNS-----CICRDSGT---DDS 55
DB 8 GSWLLALLHPTIILAQQEAVEGCSHLGQSYADRDVWKPEQCICVC--DSGVLCDI 65
QY 56 V-DTQOQQAENSVP-----TADTRSQRPDPVPRPRRGPHPR 94
DB 66 ICDDQELDCNPEIPFGCCCAVCQPPTAPTRPP-NGQPGQPK 108

RESULT 12

US-09-252-991A-28443
; Sequence 28443, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28443
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28443

Query Match 11.9%; Score 72.5; DB 4; Length 333;
Best Local Similarity 27.5%; Pred. No. 2.1; Indels 24; Gaps 3;
Matches 25; Conservative 7; Mismatches 35; Indels 24; Gaps 3;
QY 29 HFLGTGGAATTMGNSCICRDSGTSDSDVTQOQQAENSVP-----TADTRSQRPDPV 82
DB 216 HRLTGG-----DEGADEGRHHQPRQAAHRRRFLPGPDAGHRRRGAEPR 262
QY 83 P-----PRCRGPHPRKK 97
DB 263 QRTGDPAGHREAPGSLRPRRPRGHLP RRR 293

RESULT 13

US-09-252-991A-20178
; Sequence 20178, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20178
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20178

Query Match 11.7%; Score 71.5; DB 4; Length 562;
Best Local Similarity 29.7%; Pred. No. 5.5; Indels 17; Gaps 2;
Matches 22; Conservative 6; Mismatches 29; Indels 17; Gaps 2;
QY 36 AATTMGNSCICRDSGTSDSDVTQOQQAENSVPADTRSQRPDPVPRPRRGPHPR 93
DB 79 AATPAG-----EDGQLHQRRRPLAGPGSGAGACPADPRFRGRRRGAQRPPP 127
QY 94 ----RRKKQNVDL 103
DB 128 VAGSRRRSRGTDL 141

RESULT 14

US-09-252-991A-18531
; Sequence 18531, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18531
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18531

Query Match 11.7%; Score 71.5; DB 4; Length 566;
Best Local Similarity 23.6%; Pred. No. 5.6; Indels 47; Gaps 4;
Matches 29; Conservative 10; Mismatches 37; Indels 47; Gaps 4;
QY 23 LEEHIAHFLGTGGAATTMGNSC--ICRDSGTSDSDVT-----TQOQQAENSVP 71
DB 118 LERRLPFGAGGTATGRRRSCQIRVQAPGGRSVDPFGHGGPHQRRAGSGTEG 177
QY 72 DTRSQRPDP-----VPRPR-----CRGPHPR 95
DB 178 RTTRAPRPPGQQLPAGKGVQAGDRGGAQLRSPRPAAGTELLHGPARRPYR 237
QY 96 KQ 98
DB 238 RQR 240

RESULT 15

US-09-252-991A-26099
; Sequence 26099, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26099
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099

Query Match 11.7%; Score 71; DB 4; Length 863;
 Best Local Similarity 29.1%; Fred. No. 11;
 Matches 25; Conservative 8; Mismatches 33; Indels 20; Gaps 3;
 QY 31 LGTGAATT-----MNSICRDSGTDSDSYDTQOQAENS AVPTADT-----RS 75
 Db 335 LQPGTAARRTHRPWPGRGAGGDALLRPDAGQADRLRGDPRESPAQADPRAGALRAAGRR 394
 QY 76 QPRDPVRPP-----RRGRGPHEPRK 96
 Db 395 QPAVERQPPGASGLRRRRGDHRLHR 420

Search completed: April 2, 2004, 10:31:41
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:26:40 ; Search time 39 seconds
(without alignments)
946.555 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGNAFLASRLQGLL.....QNVGVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	604	99.2	576	4	Q96DX4
2	586	96.2	576	6	Q95LFP3
3	561	92.1	117	11	Q8BL58
4	556	91.3	576	11	Q8C039
5	556	91.3	576	11	Q8BVR6
6	86	14.1	601	16	Q82F17
7	85.5	14.0	230	5	Q20394
8	79.5	13.1	356	10	Q9ATR4
9	79.5	13.1	388	10	Q94IM8
10	79.5	13.1	388	10	Q8LUN6
11	79.5	13.1	388	10	Q7YIX7
12	79.5	13.1	5146	5	Q9VXR3
13	79	13.0	970	10	Q9AYF2
14	79	13.0	970	10	Q7XF23
15	78.5	12.9	188	2	Q7WX07
16	78	12.8	179	5	Q9XZ40

17	78	12.8	191	5	Q9U0C1
18	78	12.8	203	5	Q9U0C0
19	78	12.8	480	5	Q27033
20	77.5	12.7	550	12	Q40912
21	77.5	12.7	550	12	P88903
22	76.5	12.6	634	4	Q8IXW0
23	76	12.5	1063	16	Q8XXH5
24	75.5	12.4	948	5	Q9U304
25	75	12.3	147	5	Q15805
26	75	12.3	183	5	Q9U0B5
27	75	12.3	183	5	Q9U0B6
28	75	12.3	204	5	Q9U0B4
29	75	12.3	260	5	Q8IT83
30	75	12.3	267	13	Q9PUV0
31	75	12.3	278	5	Q25862
32	75	12.3	291	5	Q25789
33	74.5	12.2	121	12	Q8QRK4
34	74.5	12.2	462	3	Q42721
35	74.5	12.2	2120	5	Q8IAK1
36	74	12.2	850	16	Q8FML9
37	73.5	12.1	416	12	Q81265
38	73	12.0	206	5	Q9U0C3
39	73	12.0	220	5	Q9U0B3
40	73	12.0	222	5	Q9U0B1
41	73	12.0	353	11	Q62313
42	73	12.0	579	2	Q8GPF2
43	73	12.0	1160	5	Q8T0V9
44	73	12.0	1163	4	Q8N6U4
45	73	12.0	3571	10	Q9SL27

ALIGNMENTS

RESULT 1

Q96DX4

ID Q96DX4 PRELIMINARY; PRT; 576 AA.

AC Q96DX4; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein KIAA1972.

GN KIAA1972.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RA Strausberg R.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=21842142; PubMed=11853319;

RA Nagase T., Kikuno R., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XXII.

RT The complete sequences of 50 new cDNA clones which code for large

proteins."

RL DNA Res. 8:319-327(2001).

DR EMBL; BC013173; AAH13173.1; -

DR EMBL; AB075852; BAB85558.1; -

DR InterPro; IPR008938; ARM.

DR InterPro; IPR003877; SPRY_receptor.

DR InterPro; IPR001841; Znf_Ring.

DR Pfam; PF00622; SPRY; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00449; SPRY; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

KW Hypothetical protein_576 AA; 64180 MW; 8598E43E5691F9B CRC64;

SQ SEQUENCE

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Query Match          99.2%; Score 604; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 2
Q95LP3 PRELIMINARY; PRT; 576 AA.
AC Q95LP3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Sugano S.;
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072745; BAB69714.1; -.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64259 MW; 68D230ADIC4F5F8D CRC64;

Query Match          96.2%; Score 586; DB 6; Length 576;
Best Local Similarity 97.4%; Pred. No. 1.1e-55;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 3
Q8BLS8 PRELIMINARY; PRT; 117 AA.
AC Q8BLS8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
```

```
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK043522; BAC31566.1; -.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 12738 MW; D3FEC471ABD55D3C CRC64;

Query Match          92.1%; Score 561; DB 11; Length 117;
Best Local Similarity 91.5%; Pred. No. 9.5e-54;
Matches 107; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGAEDNVDTHQ 60
QY 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117
DB 61 QQAENSTVPTADSRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVDK 117

RESULT 4
Q8C039 PRELIMINARY; PRT; 576 AA.
AC Q8C039;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor.
GN 4930470D19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK032416; BAC27858.1; -.
DR MGD; MGI:1914860; 4930470D19RIK.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64340 MW; D72D60E803911D02 CRC64;

Query Match          91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGAEDNVDTHQ 60
QY 61 QQAENSAPVTADTRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116
DB 61 QQAENSTVPTADSRSQPRDPVPPRRGRGPHPRKKQNVGVLDTLAVIRTLVD 116

RESULT 5
Q8BVR6 PRELIMINARY; PRT; 576 AA.
ID Q8BVR6
```

Q8BVR6;
01-MAR-2003 (TREMELrel. 23, Created)
01-MAR-2003 (TREMELrel. 23, Last sequence update)
01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical Sp1a and the Ryanodine receptor (Hypothetical protein)
4930470D19RIK.
Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2234683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Besak S.A., McQuellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC STRAIN=Embryo;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076799; BAC36485.1; -
DR EMBL; BC054121; AAH54121.1; -
DR MGD; MGI:1914860; 4930470D19RIK.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR001841; Znf_Fing.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64322 MW; 823C3532FCE18387 CRC64;

Query Match 91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGNAVFLASRLSGGGLLTLEHTAHFLGTGGAATTWNSCICRDDSGTDSVDVDTQ 60
DB 1 MIVFGNAVFLASRLSGGGLLTLEHTAHFLGTGGAATTWNSCICRDDSGAENVDVTHQ 60

QY 61 QQAENSAPTADTSRQPRDPVPRPRRGKGPHEPRKKQNVGDLVLTAVIRLVD 116
DB 61 QQAENSTVPTADSRQPRDPVPRPRRGKGPHEPRKKQNVGDLVLTAVIRLVD 116

RESULT 6
Q82FI7
ID Q82FI7 PRELIMINARY; PRT; 601 AA.
AC Q82FI7;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative chitamine biosynthesis protein.
GN THIA OR SAV4265.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005038; BAC71977.1; -
DR GO; GO:0009228; P:thiamin biosynthesis; IEA.
DR InterPro; IPR002817; Thic.
DR Pfam; PF01964; Thic; 1.
DR ProDom; PD007048; Thic; 1.
DR TIGRFAMs; TIGR00190; thic; 1.
KW Complete proteome.
SQ SEQUENCE 601 AA; 66485 MW; B149CD75A602FCF5 CRC64;

Query Match 14.1%; Score 86; DB 16; Length 601;
Best Local Similarity 32.3%; Pred. No. 0.86;
Matches 31; Conservative 7; Mismatches 36; Indels 22; Gaps 4;

QY 39 TWGNSCICRDDSG--TDSVPTQQQA-----ENSAVPTADTSRQPRDPVPRP----- 83
DB 55 TWGNSVTLTSGPYTDSVPTDVRGLAPLENWIIARGTETEEVAGRFVPRPDDGDKHT 114

QY 84 -PRRGK-----PHEPRKKQNVGDLVLTAVIR 112
DB 115 SPRGGLRLNDAVFGPRGPRGPRGRDQAVTQLAVAR 150

RESULT 7
Q20394
ID Q20394 PRELIMINARY; PRT; 290 AA.
AC Q20394;
DT 01-NOV-1995 (TREMELrel. 01, Created)
DT 01-NOV-1995 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE F44D12.6 protein.
GN F44D12.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP Coles L.;

Query Match 13.1%; Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7;
 Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVDTQQAENSA-----VPTADTRSPQPRVPPRRGRGPHEP 93
 Db 179 SSVCEEDGSSLSVDGKQHQHSPADRGAGDHKGAAHGHSCKPKAPRRRAANPKPP 238

QY 94 RR 95
 Db 239 RR 240

RESULT 11

QY1X7 PRELIMINARY; PRT; 388 AA.

AC QY1X7

DT 01-OCT-2003 (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Tcosinte-branching 1.

GN TBI.

OS Oryza sativa (indica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzoideae; Oryza.

OX NCBI_TaxID=39946;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. IR-36;

RA Hu W., Zhang S., Zhao Z., Zhao Y., Sun C.R., Luo D.,

RT "The structural and expression analysis of OsTBI in rice.";

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY286002; AA37176.1.

SQ SEQUENCE 388 AA; 41504 MW; 8CF363D2EAA02743 CRC64;

Query Match

13.1%; Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7;
 Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVDTQQAENSA-----VPTADTRSPQPRVPPRRGRGPHEP 93
 Db 179 SSVCEEDGSSLSVDGKQHQHSPADRGAGDHKGAAHGHSCKPKAPRRRAANPKPP 238

QY 94 RR 95
 Db 239 RR 240

RESULT 12

Q9VXR3 PRELIMINARY; PRT; 5146 AA.

AC Q9VXR3

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE C88184 protein.

GN C88184.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasearman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A., Nunco J.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Pacleb J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Ruso S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003500; AAF48495.2;
 DR FlyBase; FBgn003067; CG8184.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.


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DR GO: 0004842; Fubiquitin-protein ligase activity; IEA.
DR GO: 0006810; P-transport; IEA.
DR GO: 0006512; P-biquitin cycle; IEA.
DR InterPro: IPR008938; ARM.
DR InterPro: IPR000569; HECT domain.
DR InterPro: IPR001993; Mitoch. carrier.
DR InterPro: IPR000449; UBA domain.
DR Pfam: PF00632; HECT; 1.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF02825; WVE; 1.
DR SMART: SM00119; HECTC; 1.
DR PROSITE: PS0237; HECT; 1.
DR PROSITE: PS00215; MITOCH. CARRIER; 1.
DR PROSITE: PS0030; UBA; 1.
SQ SEQUENCE 5146 AA; 56847 MW; 27BF187F2D279846 CRC64;

Query Match 13.1%; Score 79.5; DB 5; Length 5146;
Best Local Similarity 30.1%; Pred. No. 54;
Matches 22; Conservative 8; Mismatches 30; Indels 13; Gaps 2;

QY 32 GTGGAATTGNSCICRDSGTDSDVDTQOQAENSAPVTDTRSQPRDPVPRRGRGPH 91
DB 853 GTGSASSVLQGAADTNDSDGDDDDDDSSA-----SQOQQQTTPGQGGPS 901

QY 92 EPRKKQNVGLV 104
DB 902 TPR--TQAGGV 912

RESULT 13
ID Q9AYF2 PRELIMINARY; PRT; 970 AA.
AC Q9AYF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Zea mays chromosome 422kDazein-associated intercluster
DE region, copia-type polypolyprotein.
GN OSJNBA0094J09.18.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RT "Genomic Sequence For Oryza sativa, Nipponbare strain, Chromosome X,
RT Clone OSJNBA0094J09, complete sequence."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: ACU78839; AAK13102.1; -.
DR Gramene; Q9AYF2; -.
DR GO: 0003677; F:DNA binding; IEA.
DR GO: 0004289; F:subtilase activity; IEA.

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DR GO: 0006310; P:DNA recombination; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000209; Peptidase_S8.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00665; rve; 1.
DR PROSITE: PS00136; SUBTILASE ASP; 1.
SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match 13.0%; Score 79; DB 10; Length 970;
Best Local Similarity 27.4%; Pred. No. 8;
Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGWAVFLASRLG----QGLLTLEHIAHFGLT-----GGAATTM--GNSCICRDD 49
DB 551 YSWVFFMATKDEAFQHFRGLFLD---LEFPGLKRIKIRSDNGTUSQVGEDSCIFEDD 607

QY 50 SGTDDSDVDTQOQAENSAPVTDTRSQPRDPVPRRGRGPHPRRKKQNVG 102
DB 608 SDDDDKVGSGAGTGRAGQTAST-----PP--GRPPQDERSNRPGSSG 649

RESULT 14
ID Q7XF23 PRELIMINARY; PRT; 970 AA.
AC Q7XF23;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Zea mays chromosome 422kDazein-associated intercluster
DE region, copia-type polypolyprotein.
GN OSJNBA0094J09.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017089; AAP53536.1; -.
KW Polyprotein.
SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match 13.0%; Score 79; DB 10; Length 970;
Best Local Similarity 27.4%; Pred. No. 8;
Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGWAVFLASRLG----QGLLTLEHIAHFGLT-----GGAATTM--GNSCICRDD 49
DB 551 YSWVFFMATKDEAFQHFRGLFLD---LEFPGLKRIKIRSDNGTUSQVGEDSCIFEDD 607

QY 50 SGTDDSDVDTQOQAENSAPVTDTRSQPRDPVPRRGRGPHPRRKKQNVG 102
DB 608 SDDDDKVGSGAGTGRAGQTAST-----PP--GRPPQDERSNRPGSSG 649

RESULT 15
ID Q7WX07 PRELIMINARY; PRT; 188 AA.
AC Q7WX07;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative single-strand binding protein.

```

GN SSB OR PHG335.
 OS Alcalligenes eutrophus (Ralstonia eutropha).
 OG Plasmid megaplasmid pHG1.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=H16;
 RC Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
 RA Gottschalk G.;
 RT "Complete Nucleotide Sequence of pHG1: A Ralstonia eutropha H16
 RT Megaplasmid Encoding Key Enzymes Of H2-based Lithoautotrophy and
 RT Anaerobiosis";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY305378; AAF86084.1; -.
 KW Plasmid.
 SQ SEQUENCE 188 AA; 20451 MW; B43832FBCC232CF4 CRC64;
 Query Match 12.9%; Score 78.5; DB 2; Length 188;
 Best Local Similarity 33.8%; Pred.No.1.5; Indels 13; Gaps 5;
 Matches 26; Conservative 8; Mismatches 30;
 Qy 32 GTGGAATTGNSCTCRDSDGTDSDVTQQQAENSAYPTADTSQP--RDPVRRPRGRG 89
 Db 110 GRGASD--GDS-----DSGTDRSASQSPASQARSAPTGG-RQPPARRQPAQPPSNGFG 161
 Qy 90 PHE---PRKKQNVGDL 103
 Db 162 DFNEDIFARPALDGI 178

Search completed: April 2, 2004, 10:30:33
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:26:10 ; Search time 17 Seconds
(without alignments)
358.365 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGWAVFLASRLSQGLL.....QNVGVLDTLAVITLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	13.0	612	1	THIC_STRCO
2	78.5	12.9	188	1	SSB_ALCEU
3	78	12.8	1483	1	BALB_HUMAN
4	75	12.3	286	1	MSA2_PLAF1
5	73.5	12.1	2505	1	CCAA_HUMAN
6	73	12.0	281	1	MSA2_PLAFH
7	73	12.0	353	1	TGNI_MOUSE
8	73	12.0	1466	1	CAL3_HUMAN
9	72.5	11.9	282	1	MSA2_PLAF2
10	72.5	11.9	272	1	MSA2_PLAF7
11	72.5	11.9	274	1	MSA2_PLAF6
12	72.5	11.9	287	1	MSA2_PLAFG
13	72.5	11.9	300	1	MSA2_PLAFI
14	72.5	11.9	300	1	MSA2_PLAFZ
15	72.5	11.9	302	1	MSA2_PLAF9
16	72.5	11.9	347	1	MSA2_PLAF2
17	72.5	11.9	458	1	YNEI_CABEL
18	72	11.8	1787	1	CHD3_CABEL
19	71	11.7	1479	1	BALB_MOUSE
20	70.5	11.6	3726	1	TRX_DROME
21	70	11.5	445	1	NRH3_MOUSE
22	69	11.3	1944	1	CHD3_HUMAN
23	68	11.2	424	1	COT1_BOVIN
24	68	11.2	445	1	NRH3_RAT
25	68	11.2	504	1	FTSY_SYNY3
26	68	11.2	702	1	EXO1_YEAST
27	67.5	11.1	399	1	SIR3_HUMAN
28	67.5	11.1	727	1	CTCF_HUMAN
29	67.5	11.1	1298	1	ICP4_HSV1
30	67	11.0	393	1	CIM4_HUMAN
31	67	11.0	1202	1	NOS3_HUMAN
32	67	11.0	3828	1	TRX_DROVI
33	66.5	10.9	217	1	YKR4_EBV

34	66.5	10.9	268	1	EP34_HCMVA	P16768 human cytom
35	66.5	10.9	276	1	MSA2_PLAF8	Q99320 plasmodium
36	66.5	10.9	343	1	GLN2_STRVR	P19432 streptomyc
37	66.5	10.9	423	1	COT1_HUMAN	P10589 homo sapien
38	66.5	10.9	684	1	EP84_HCMVA	P17151 human cytom
39	66	10.8	228	1	EPAS_HUMAN	P52803 homo sapien
40	66	10.8	228	1	EPAS_MOUSE	O08543 mus muscucu
41	66	10.8	324	1	HE31_STRAW	Q82676 streptomyc
42	66	10.8	736	1	DVL2_XENLA	P31142 xenopus lae
43	66	10.8	1021	1	MAPA_MOUSE	Q9qy76 mus muscucu
44	66	10.8	1380	1	CYAA_LEIDO	Q27675 leishmania
45	66	10.8	2716	1	OSA_DROME	Q8in94 drosophila

ALIGNMENTS

RESULT 1

ID	THIC_STRCO	STANDARD	PRT	612 AA.
AC	Q9X9U0			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Thiamine biosynthesis protein thic.			
GN	THIC OR SCO3928 OR SCQ11.11.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomycetes.			
OX	NCBI_taxid=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3(2) / M145;			
RA	MEDLINE=21996410; PubMed=12000953;			
RA	Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,			
RA	Thomson N.R., James K.D., Brown S., Chandra G., Chen C.W., Collins M.,			
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,			
RA	Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,			
RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,			
RA	Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,			
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,			
RA	Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,			
RA	Hopwood D.A.,			
RA	"Complete genome sequence of the model actinomycete Streptomycetes			
RT	coelicolor A3(2).";			
RL	Nature 417:141-147(2002).			
CC	FUNCTION: Required for the synthesis of the hydromethylpyrimidine			
CC	(HMP) moiety of thiamine (4-amino-2-methyl-5-			
CC	hydroxymethylpyrimidine) (By similarity).			
CC	PATHWAY: Thiamine biosynthesis.			
CC	SIMILARITY: Belongs to the thic family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AL939118; CAB46966.1; -.			
DR	PIR; T37181; T37181.			
DR	HANAP; MF_00089; -; 1.			
DR	InterPro; IPR002817; Thic.			
DR	Pfam; PF01964; thic; 1.			
DR	ProDom; PD007048; Thic; 1.			
DR	TIGRFAMs; TIGR00190; thic; 1.			
KW	Thiamine biosynthesis; Complete proteome.			
SQ	SEQUENCE 612 AA; 67371 MW; 230BF254200CF68 CRC64;			

Query Match 13.0%; Score 79; DB 1; Length 612;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

```

QY 39 TWGNSICRDSG--TDSVDTQQQQA-----ENSAVTAATRSQPRDPVRP----- 83
DB 60 TNGQSVTLTYDTSGPYTDLVDTRGLAPLRENWIIARGDTEBYAGRPVPEFDGKHT 119
QY 84 -PRRGGRG-----PHEPRKKQNVGLVLDLTAVIR 112
DB 120 SPRGGLNLDVFPGRPRQPRGRDGNVQLAYAR 155

RESULT 2
SSB ALCEU
ID SSB ALCEU STANDARD; PRT; 188 AA.
AC P5927; Q7WX07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Single-strand binding protein (SSB) (Helix-destabilizing protein).
GN SSB OR PHG335.
OS Algaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H16 / DSM 428 / ATCC 17699;
RA Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
RA Gottschalk G.;
RT "Complete nucleotide sequence of pHG1: a Ralstonia eutropha H16
RT megaplasmid encoding key enzymes of H2-based lithoautotrophy and
RT anaerobiosis.";
RL J. Mol. Biol. 332:369-383(2003).
CC -!- FUNCTION: This protein is essential for replication of the
CC chromosome. It is also involved in DNA recombination and repair
CC (By similarity).
CC -!- SIMILARITY: Contains 1 SSB domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AY305378; AAP86084.1; -.
KW PROSITE; P550935; SSB; 1.
FT DOMAIN 4 109
FT SEQUENCE 188 AA; 20451 MW; B43832PBC232CF4 CRC64;
Query Match 12.9%; Score 78.5; DB 1; Length 188;
Best Local Similarity 33.8%; Pred. No. 0.71;
Matches 26; Conservative 8; Mismatches 30; Indels 13; Gaps 5;

QY 32 GTGGATATWNSICRDSGTDSDVDTQQQQAENSAVTAATRSQPR--RDPVPRRGGRG 89
DB 110 GRGGASD--GDS-----DSGTRDSAQSPASQAQSAPTQ--RQPPARRQPAQPPSNGFG 161
QY 90 PHE---PRRKQNVGL 103
DB 162 DFNEIDIPFAPRALDGI 178

RESULT 3
BALB HUMAN
ID BALB HUMAN STANDARD; PRT; 1483 AA.
AC Q9UIG0; O95039; O95247; O95277;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bromodomain adjacent to zinc finger domain protein 1B (Williams-Beuren

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DE syndrome chromosome region 9 protein) (WBSR9) (Williams syndrome
DE transcription factor) (hWALP2).
GN BAZ1B OR WBSR9 OR WSC10 OR WSTF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=9907764; PubMed=9858827;
RA Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
RT Identification of the WBSR9 gene, encoding a novel transcriptional
RT regulator, in the Williams-Beuren syndrome deletion at 7q11.23.;
RL Cytogenet. Cell Genet. 82:238-246(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99047530; PubMed=9828126;
RA Lu X., Meng X., Morris C.A., Keating M.T.;
RT "A novel human gene, WSTF, is deleted in Williams Syndrome.";
RL Genomics 54:241-249(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX TISSUE=Testis;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes.";
RL Genomics 63:40-45(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX Minx P., Graves T., Duckels G., Harrison M., Waterston R.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=21977304; PubMed=11980720;
RA Bozhernok L., Wade P.A., Varga-Weisz P.;
RT "WSTF-ISWI chromatin remodeling complex targets heterochromatic
RT replication foci.";
RL EMBO J. 21:2231-2241(2002).
CC -!- FUNCTION: Forms a chromatin remodeling complex that mobilizes
CC nucleosomes and reconfigures irregular chromatin to a regular
CC nucleosomal array structure.
CC -!- SUBUNIT: Interacts with ISWI (imitation SWI protein) to form the
CC WSTF-ISWI chromatin remodeling complex (WICH).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential). Accumulates in
CC pericentromeric heterochromatin during replication.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UIG0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UIG0-2; Sequence=VSP_000552;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with high levels of
CC expression in heart, brain, placenta, skeletal muscle and ovary.
CC -!- DEVELOPMENTAL STAGE: Expressed at equal levels in 19-23 weeks old
CC fetal tissues.
CC -!- DISEASE: Haploinsufficiency of BAZ1B may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC -!- SIMILARITY: Belongs to the WAL family.
CC -!- SIMILARITY: Contains 1 bromodomain.
CC -!- SIMILARITY: Contains 1 DDT domain.
CC -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC -!- SIMILARITY: Contains 1 WAC domain.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in positions 1031, 1042 and 1422.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 1478.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC EMBL; AF084479; AAD08675.1; -;
 DR EMBL; AF072810; AAC97879.1; ALT FRAME.
 DR EMBL; AB032253; BAA89210.1; ALT FRAME.
 DR EMBL; AC005074; AAD04720.1; ALT SEQ.
 DR EMBL; AC005089; -; NOT_ANNOTATED_CDS.
 DR HSP; O92831; 1891.
 DR TRANSFAC; T04145; -;
 DR Genew; HGNC:961; BAZ1B.
 DR MIN; 605681; -;
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003700; F:transcription factor activity; NAS.
 DR GO; GO:000270; F:zinc ion binding; NAS.
 DR GO; GO:0006350; P:transcription; NAS.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR004022; DDT_dom.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF00439; bromodomain; 1.
 DR Pfam; PF00628; PHD; 1.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00297; BROMO; 1.
 DR SMART; SM00521; DDT; 1.
 DR SMART; SM00249; PHD; 1.
 DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
 DR PROSITE; PS0014; BROMODOMAIN_2; 1.
 DR PROSITE; PS00827; DDT; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 1.
 DR PROSITE; PS00016; ZF_PHD_2; 1.
 KW Transcription regulation; Bromodomain; Zinc-finger; Coiled coil;
 KW Nuclear protein; Alternative splicing; Williams-Seuren syndrome.
 FT DOMAIN 20 126
 FT DDT 604 668
 FT ZN_FING 1184 1234 PHD-TYPE.
 FT DOMAIN 1356 1426 BROMODOMAIN.
 FT DOMAIN 306 578 LYS-RICH
 FT DOMAIN 533 586 COILED COIL (POTENTIAL).
 FT DOMAIN 768 814 COILED COIL (POTENTIAL).
 FT DOMAIN 850 893 COILED COIL (POTENTIAL).
 FT DOMAIN 1245 1283 COILED COIL (POTENTIAL).
 FT DOMAIN 1261 1273 POLY-GLU.
 FT VARSPIC 660 663 Missing (in isoform 2).
 FT CONFLICT 14 14 /Ptd-VP 000552.
 FT CONFLICT 22 22 K -> N (IN REF. 3).
 FT CONFLICT 136 136 L -> F (IN REF. 3).
 FT CONFLICT 191 191 K -> E (IN REF. 1).
 FT CONFLICT 298 298 N -> D (IN REF. 4).
 FT CONFLICT 823 823 Y -> V (IN REF. 4).
 FT CONFLICT 823 823 E -> R (IN REF. 3).
 FT CONFLICT 1191 1191 R -> P (IN REF. 2).
 FT CONFLICT 1354 1354 K -> M (IN REF. 2).
 FT CONFLICT 1438 1438 A -> V (IN REF. 3).
 SQ SEQUENCE 1483 AA; 170902 MW; 0CC146FEB954261 CRC64;

Query Match 12.8%; Score 78; DB 1; Length 1483;
 Best Local Similarity 27.5%; Pred. No. 8;
 Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;
 QY 48 DSGTDSVDTQQQAENSVAFTADTRSQRPDPVR-----PP-----RRGQFHPRR 95
 Db 1255 EDDSEDEEEEDVEVAGLRPRKTRKHSVIPAARSGRPGKXPHSTR 1314
 QY 96 KK-----QNVGLVLT 107
 Db 1315 SQKAPPVDDAEVDLVLT 1334

RESULT 4

MSA2_PLAF1 STANDARD; PRT; 286 AA.
 ID MSA2_PLAF1
 AC P50496;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface antigen 2 precursor (MSA-2).
 GN MSA2.
 OS Plasmodium falciparum (isolate 311).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN NCBI_TaxID=57265;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9217826; PubMed=1542312;
 RA Marshall V.M.; Coppel R.L.; Anders R.F.; Kemp D.J.;
 RT "Two novel alleles within subfamilies of the merozoite surface
 antigen 2 (MSA-2) of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 50:181-194(1992).
 CC -!- FUNCTION: May play a role in the merozoite attachment to the
 CC erythrocyte.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 CC EMBL; M73809; AAA29697.1; -;
 DR InterPro; IPR001136; MSA_2.
 DR Pfam; PF00985; MSA_2; 1.
 KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KW GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT CHAIN 21 262
 FT PROPEP 263 286
 FT DOMAIN 44 212
 FT DOMAIN 115 122 POLY-THR.
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 286 AA; 28844 MW; D1F4947CE68D5805 CRC64;
 Query Match 12.3%; Score 75; DB 1; Length 286;
 Best Local Similarity 34.6%; Pred. No. 2.5;
 Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;
 QY 32 GTGGA-----ATTMGNSICRDBSDSGTDDSV-----DT-----QQQAENSVAFTADT 73
 Db 147 GNGVQKPNQANKETQNNNV-QDSQTSKSNVPTQDADTKSPTAQPEQAENSA-PTAEQ 204
 QY 74 RSQRPDPVPRPRGRGPH 91
 Db 205 TESPELQSAPEKNKGQGH 222
 RESULT 5
 CCAA_HUMAN STANDARD; PRT; 2505 AA.
 ID CCAA_HUMAN
 AC Q00555; P78510; P78511; Q16290; Q92690; Q99790; Q99791; Q99792;
 AC Q99793;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent P/Q-type calcium channel alpha-1A subunit. (Calcium

DE channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel
DE 1) (BI).
GN CACNA1A OR CACNA1A4 OR CACNA1A OR CACNA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1].
RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
RC TISSUE=Neuron;
RX MEDLINE=99158614; PubMed=10049321;
RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
RA Harold M.M., Johnson E.C., Williams M.E.;
RT "Structural elements in domain IV that influence biophysical and
RT pharmacological properties of human alpha1A-containing high-voltage-
RT activated calcium channels.";
RL Biophys. J. 76:1384-1400(1999).
RN [2].
RP SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
RC TISSUE=Cerebellum;
RX MEDLINE=97053792; PubMed=8898206;
RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
RA Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,
RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
RA Ferrari M.D., Frants R.R.;
RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
RT mutations in the Ca_v2.4 channel gene CACNA1A.";
RL Cell 87:543-552(1996).
RN [3].
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=97141920; PubMed=8988170;
RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
RT channel.";
RL Nat. Genet. 15:62-69(1997).
RN [4].
RP SEQUENCE OF 1233-1651 FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowroneki E., Adamson A.W.,
RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stiiwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomerly M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [5].
RP SEQUENCE OF 1693-1807 FROM N.A.
RC TISSUE=Lung carcinoma;
RX MEDLINE=95123449; PubMed=7823133;
RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;
RT "Expression and antibody inhibition of P-type calcium channels in
RT human small-cell lung carcinoma cells.";
RL J. Neurosci. 15:274-283(1995).
RN [6].
RP SEQUENCE OF 2038-2258 FROM N.A.
RC TISSUE=Frontal cortex;
RX MEDLINE=96102310; PubMed=8525433;
RA Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
RA McInnis M.G., Ross C.A.;
RT "Characterization of cDNA clones containing CCA trinucleotide repeats
RT derived from human brain.";
RL Somat. Cell Mol. Genet. 21:279-284(1995).
CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. The isoform alpha-1A
CC gives rise to P and/or Q-type calcium currents. P/Q-type calcium
CC channels belong to the "high-voltage activated" (HVA) group and

are blocked by the funnel toxin (Ftx) and by the omega-agatoxin-
IVA (omega-Aga-IVA). They are however insensitive to
dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTX-GVIA).
-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
Name=BI-1-GCAG; Synonyms=1A-1;
IsoId=O00555-1; Sequence=Displayed;
Name=BI-1; Synonyms=1A-2;
IsoId=O00555-2; Sequence=VSP_000875;
Name=BI-1(V1);
IsoId=O00555-3; Sequence=VSP_000871, VSP_000875;
Name=BI-1(V1)-GCAG;
IsoId=O00555-4; Sequence=VSP_000871;
Name=BI-1(V2);
IsoId=O00555-5; Sequence=VSP_000872;
Name=BI-1(V2)-GCAG;
IsoId=O00555-6; Sequence=VSP_000872;
Name=BI-1(V2 V3);
IsoId=O00555-7; Sequence=VSP_000873, VSP_000874;
-1- TISSUE SPECIFICITY: Brain specific; mainly found in cerebellum,
cerebral cortex, thalamus and hypothalamus. No expression in
heart, kidney, liver or muscle. Purkinje cells contain
predominantly P-type VSCC, the Q-type being a prominent calcium
current in cerebellar granule cells.
-1- DOMAIN: Each of the four internal repeats contains five
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
positively charged transmembrane segment (S4). S4 segments
probably represent the voltage-sensor and are characterized by a
series of positively charged amino acids at every third position.
-1- POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic: 6 to
17 repeats in the normal population, expanded to about 21 to 30
repeats in spinocerebellar ataxia 6 (SCA6) patients. There seems
to be a correlation between the repeat number and earlier onset of
the disorder.
-1- DISEASE: Defects in CACNA1A are the cause of spinocerebellar
ataxia type 6 (SCA6) [MIM:183086]. SCA6 is an autosomal dominant
disorder characterized by slowly progressive cerebellar ataxia of
the limbs and gait, dysarthria, nystagmus, and mild vibratory and
proprioceptive sensory loss. These symptoms are probably explained
by severe loss of cerebellar Purkinje cells. SCA6 is caused by
expansion of a CAG repeat in the coding region of CACNA1A.
-1- DISEASE: Defects in CACNA1A are the cause of familial hemiplegic
migraine (FHM) [MIM:141500]; also known as migraine familial
hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype of
migraine with aura, is associated with ictal hemiparesis and, in
some families, progressive cerebellar atrophy.
-1- DISEASE: Defects in CACNA1A are the cause of episodic ataxia type
2 (EA-2) [MIM:108500]; also known as acetazolamide-responsive
hereditary paroxysmal cerebellar ataxia (APCA). This autosomal
dominant disorder is characterized by acetazolamide-responsive
attacks of cerebellar ataxia and migraine-like symptoms,
interictal nystagmus, and cerebellar atrophy.
-1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.

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EMBL; AF004884; AAB61613.1; -.

EMBL; AF004883; AAB61612.1; --
 DR EMBL; X98987; CAA68172.1; --
 DR EMBL; Z80114; -- NOT_ANNOTATED_CDS.
 DR EMBL; Z80115; -- NOT_ANNOTATED_CDS.
 DR EMBL; U79665; AAB64179.1; -- ALT INIT.
 DR EMBL; U79665; AAB49674.1; -- ALT INIT.
 DR EMBL; U79665; AAB49675.1; -- ALT INIT.
 DR EMBL; U79665; AAB49676.1; -- ALT INIT.
 DR EMBL; U79667; AAB49677.1; -- ALT INIT.
 DR EMBL; U79668; AAB49678.1; -- ALT INIT.
 DR EMBL; AC005305; AAC26839.1; --
 DR EMBL; S76537; AAB33068.1; --
 DR EMBL; U06702; -- NOT_ANNOTATED_CDS.
 DR Genew; HGNC:1388; CACNALA.
 DR MIM; 601011; --
 DR MIM; 183086; --
 DR MIM; 141500; --
 DR MIM; 108500; --
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002077; Ca_channel_alpha.
 DR InterPro; IPR002111; Cat_channel_TpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR005448; PQVDCALpha1.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHANNEL.
 DR PRINTS; PR01632; PQVDCALPHA1.
 DR KEGG; K01632; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 KW Disease mutation; Triplet repeat expansion.
 FT REPEAT 85 363
 FT REPEAT 473 717
 FT REPEAT 1231 1514
 FT REPEAT 1551 1814
 FT DOMAIN 1 98
 FT TRANSFEM 99 117
 FT TRANSFEM 118 135
 FT TRANSFEM 136 155
 FT TRANSFEM 156 167
 FT TRANSFEM 168 185
 FT TRANSFEM 186 190
 FT TRANSFEM 191 209
 FT TRANSFEM 210 228
 FT TRANSFEM 229 248
 Query Match 12.1%; Score 73.5; DB 1; Length 2505;
 Best Local Similarity 24.2%; Pred. No. 41;
 Matches 31; Conservative 9; Mismatches 39; Indels 49; Gaps 4;
 QY 12 SRSLGQGLLTLEHIAHFLGTGG-----AATTWNSC-----44
 DB 2247 SRSPSEG-----REHMAHQSSSVSPAPSTGTSPPRRGRQLPQETSTPRPHVSYS 2301
 QY 45 -ICRDSGTDSDVTQQQQAENSVA-----PTADTRSPDRPVRPREG 87
 DB 2302 PVIRKAGSGPPQQQQQQQQQAVAPGRAATSPRRYPGPTAEPLAGDRPPTGGHSSG 2361
 QY 88 RGPHEPR 95
 DB 2362 RSPRMER 2369
 RESULT 6
 MSA2_PLAFH
 ID MSA2_PLAFH STANDARD; PRT; 281 AA.
 AC Q99319;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 3).

GN MSA2.
 OS Plasmodium falciparum (isolate thtn / Thailand).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=70151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91219803; PubMed=2090943;
 RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
 RT "Sequence comparison of allelic forms of the Plasmodium falciparum
 merozoite surface antigen MSA2.";
 RL Mol. Biochem. Parasitol. 43:211-220(1990).
 CC -!- FUNCTION: May play a role in the merozoite attachment to the
 CC erythrocyte.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
 CC
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 CC
 CC EMBL; M60189; AAA29689.1; --
 DR InterPro; IPR001136; MSA_2.
 DR Pfam; PF00985; MSA_2; 1.
 KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KW GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT CHAIN 21 257
 FT PROPEP 258 281
 FT DOMAIN 44 207
 FT DOMAIN 111 118
 FT CARBOHYD 22 22
 FT CARBOHYD 36 36
 FT CARBOHYD 158 158
 FT CARBOHYD 230 230
 FT CARBOHYD 254 254
 FT CARBOHYD 255 255
 FT SEQUENCE 281 AA; 28892 MW; 50598AA42D64CCBC CRC64;
 Query Match 12.0%; Score 73; DB 1; Length 281;
 Best Local Similarity 35.8%; Pred. No. 4;
 Matches 24; Conservative 6; Mismatches 25; Indels 12; Gaps 3;
 QY 36 AATTWNSCICRDSGTDSDV-----DT-----QQQAENSVAPTADTRSPDRPVRP 84
 DB 152 ANTEQNNSNVQDSQTSKSNVPTQADATKSTPAQPEQAENSA-PTAEQTSPQLQSAPE 210
 QY 85 RRGGRPH 91
 DB 211 NKGTCQH 217
 RESULT 7
 TGN1_MOUSE
 ID TGN1_MOUSE STANDARD; PRT; 353 AA.
 AC Q62313.
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Trans-golgi network integral membrane protein 1 precursor (TGN38A).
 GN TGNL1 OR TGN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;

RX MEDLINE=95301533; PubMed=7540170;
 RA Kasai K., Takahashi S., Murakami K., Nakayama K.;
 RT "Strain-specific presence of two TGN38 isoforms and absence of TGN41
 RT in mouse.";
 RL J. Biol. Chem. 270:14471-14476 (1995).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, and Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chochia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gusincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu L.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Ahteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield Y.S.N., Krzywinski M.F., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May be involved in regulating membrane traffic to and
 CC from trans-Golgi network.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Primarily in trans-
 CC Golgi network. Cycles between the trans-Golgi network and the cell
 CC surface returning via endosomes (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- MISCELLANEOUS: Also found in strains BALB/c, C57BL/6 and DBA/2.
 CC
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 CC
 DR EMBL; D50031; BAA08757.1; -;
 DR EMBL; AK041302; BAC30896.1; -;
 DR EMBL; AK076586; BAC38404.1; -;
 DR EMBL; BC009143; AA09143.1; -;
 DR PIR; B56940; B56940.
 DR MGD; MGI:105080; Tgoln1.
 KW Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 353 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE
 FT PROTEIN 1.
 FT DOMAIN 18 298 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 299 319 POTENTIAL.
 FT DOMAIN 320 353 CYTOPLASMIC (POTENTIAL).
 FT SITE 346 349 ENDOCYTOSIS SIGNAL (BY SIMILARITY).
 FT DOMAIN 131 178 6 X 8 AA TANDEM REPEATS.
 FT REPEAT 131 138 1.
 FT REPEAT 139 146 2.
 FT REPEAT 147 154 3.
 FT REPEAT 155 162 4.
 FT REPEAT 163 170 5.
 FT REPEAT 171 178 6.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 353 AA; 37848 MW; 95C340C2F4A21EB3 CRC64;
 Query Match 12.0%; Score 73; DB 1; Length 353;
 Best Local Similarity 30.5%; Pred. NO. 5.1;
 Matches 18; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
 QY 32 GTGGAATTGNSICRDSSTDSVDTQQQAENSAVPTADTRSQPRDVPVRRGRGP 90
 DB 148 GDSGKTEAGSNKATDDSGKTKVLDLRPTSKIS-----PDTESTKTKVQTEKGQKP 202
 RESULT 8
 CAL3 HUMAN STANDARD; PRT; 1466 AA.
 ID P22461; Q15112;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1 (III) chain precursor.
 GN COL3A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=89350838; PubMed=2764886;
 RA Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
 RA Prockop D.J.;
 RT "Structure of cDNA clones coding for the entire prepro alpha 1 (III)
 RT chain of human type III procollagen. Differences in protein structure
 RT from type I procollagen and conservation of codon preferences.";
 RL Biochem. J. 260:509-516 (1989).
 RN [2]
 RP SEQUENCE OF 149-1225 FROM N.A.
 RX MEDLINE=89386015; PubMed=2780304;
 RA Janeczko R.A., Ramirez F.;
 RT "Nucleotide and amino acid sequences of the entire human alpha 1
 RT (III) collagen.";
 RL Nucleic Acids Res. 17:6742-6742 (1989).
 RN [3]
 RP SEQUENCE OF 168-398.
 RX MEDLINE=77134724; PubMed=557335;
 RA Seyer J.M., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of cyanogen

RT bromide peptides from the amino-terminal segment of type III collagen
RL of human liver." ;
RN Biochemistry 16:1158-1164(1977).
RP [4]
RA SEVER J.M.;
RA Submitted (DEC-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 399-727.
RX MEDLINE=79000343; PubMed=687591;
RA SEYER J.M., Kang A.H.;
RA "Covalent structure of collagen: amino acid sequence of five
RT consecutive CNBr peptides from type III collagen of human liver." ;
RL Biochemistry 17:3404-3411(1978).
RN [6]
RP SEQUENCE OF 728-964.
RX MEDLINE=8019828; PubMed=6246925;
RA SEYER J.M., Mainardi C., Kang A.H.;
RA "Covalent structure of collagen: amino acid sequence of alpha 1
RT (III)-CB5 from type III collagen of human liver." ;
RL Biochemistry 19:1583-1589(1980).
RN [7]
RP SEQUENCE OF 950-1466 FROM N.A.
RX MEDLINE=88189827; PubMed=3357782;
RA Mankoo B.S., Dalglish R.;
RA "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end." ;
RL Nucleic Acids Res. 16:2337-2337(1988).
RN [8]
RP REVISION TO 1184.
RX MEDLINE=89098346; PubMed=3211760;
RA Molyneux K., Dalglish R.;
RA "Human type III collagen 'variant' is a cDNA cloning artefact." ;
RL Nucleic Acids Res. 16:11833-11833(1988).
RN [9]
RP SEQUENCE OF 1065-1466 FROM N.A.
RX MEDLINE=85087944; PubMed=6096827;
RA Rosenthal H.R., Brinker J.W., May M., Pihlajaniemi T., Morrow S.,
RA Rosenbloom J., Myers J.C.;
RA "Molecular cloning and carboxyl-propeptide analysis of human type III
RT procollagen." ;
RL Nucleic Acids Res. 12:9383-9394(1984).
RN [10]
RP SEQUENCE OF 965-1200.
RX MEDLINE=81208139; PubMed=7016180;
RA SEYER J.M., Kang A.H.;
RA "Covalent structure of collagen: amino acid sequence of alpha
RT 1(III)-CB9 from type III collagen of human liver." ;
RL Biochemistry 20:2621-2627(1981).
RN [11]
RP SEQUENCE OF 1176-1466 FROM N.A.
RX MEDLINE=85157600; PubMed=2579949;
RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
RA "Isolation of cDNA and genomic clones encoding human pro-alpha 1
RT (III) collagen. Partial characterization of the 3' end region of the
RT gene." ;
RL J. Biol. Chem. 260:4357-4363(1985).
RN [12]
RP SEQUENCE OF 1161-1200 FROM N.A.
RX MEDLINE=86187804; PubMed=3754462;
RA Miskulin M., Dalglish R., Klueve-Beckerman B., Rennard S.I.,
RA Tolstoehev P., Brantly M., Crystal R.G.;
RA "Human type III collagen gene expression is coordinately modulated
RT with the type I collagen genes during fibroblast growth." ;
RL Biochemistry 25:1408-1413(1986).
RN [13]
RP SEQUENCE OF 1-170 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88303360; PubMed=3405773;
RA Tonan D., Ricca G., de Crombrughe B.; for the amino-terminal region
RT "Nucleotide sequence of a cDNA coding for the amino-terminal region
RT of human prepro alpha 1(III) collagen." ;
RL Nucleic Acids Res. 16:7201-7201(1988).
RN [14]
RP SEQUENCE OF 1-176 FROM N.A.
RX MEDLINE=89378752; PubMed=2777083;
RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
RA "Cloning and analysis of the 5' portion of the human type-III
RT procollagen gene (COL3A1)." ;
RL Gene 78:255-265(1989).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=9101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RA "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels." ;
RL Hum. Mutat. 9:300-315(1997).
RN [16]
RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.
RX MEDLINE=93293988; PubMed=8514866;
RA Tromp G., Wu Y., Prockop D.J., Madhathi S.L., Kleinert C.,
RA Barley J.J., Zhuang J., Noerregaard C., Darling R.C., Abbott W.M.,
RA Cole C.W., Jaakkola P., Rytynen M., Pearce W.H., Yao J.S.T.,
RA Majamaa K., Smulders S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
RA Jackson C.B., Michels V.V., Kaye M., Kuivaniemi H.;
RA "Sequencing of cDNA from 50 unrelated patients reveals that mutations
RT in the triple-helical domain of type III procollagen are an
RT infrequent cause of aortic aneurysms." ;
RL J. Clin. Invest. 91:2539-2545(1993).
RN [17]
RP VARIANT THR-698.
RX MEDLINE=91045136; PubMed=2235526;
RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,
RA Wu Y., Ganguly A., Prockop D.J.;
RA "G to A polymorphism in exon 31 of the COL3A1 gene." ;
RL Nucleic Acids Res. 18:6180-6180(1990).
RN [18]
RP VARIANT AORTIC ANEURYSM ARG-786.
RX MEDLINE=91056145; PubMed=2243125;
RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
RA "A mutation in the gene for type III procollagen (COL3A1) in a family
RT with aortic aneurysms." ;
RL J. Clin. Invest. 86:1465-1473(1990).
RN [19]
RP VARIANT EDS-IV ARG-828.
RX MEDLINE=94016385; PubMed=8411057;
RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
RA "The substitution of glycine 661 by arginine in type III collagen
RT produces mutant molecules with different thermal stabilities and
RT causes Ehlers-Danlos syndrome type IV." ;
RL J. Med. Genet. 30:690-693(1993).
RN [20]
RP VARIANT EDS-IV SER-957.
RX MEDLINE=89109135; PubMed=2492273;
RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
RA "A single base mutation that substitutes serine for glycine 790 of
RT the alpha 1 (III) chain of type III procollagen exposes an arginine
RT and causes Ehlers-Danlos syndrome IV." ;
RL J. Biol. Chem. 264:1349-1352(1989).
RN [21]
RP VARIANT EDS-IV VAL-960.
RX MEDLINE=95268429; PubMed=7749417;
RA Tromp G., de Paeppe A., Nuytink L., Madhathi S.L., Kuivaniemi H.;
RA "Substitution of valine for glycine 793 in type III procollagen in
RT Ehlers-Danlos syndrome type IV." ;
RL Hum. Mutat. 5:179-181(1995).
RN [22]
RP VARIANT EDS-IV GLU-1014.
RX MEDLINE=92316511; PubMed=1352273;
RA Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
RA Pope F.M.;
RA "A single base mutation in the gene for type III collagen (COL3A1)
RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos
RT syndrome type IV. An unaffected family member is mosaic for the
RT mutation." ;
RL Hum. Genet. 89:414-418(1992).

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	238	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	239	262	HYDROPHOBIC, REMOVED DURING MATURATION
FT				(BY SIMILARITY).
FT	DOMAIN	44	188	POLYMORPHIC REGION.
FT	DOMAIN	91	98	POLY-THR.
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	236	236	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	SEQUENCE	262 AA;	27374 MW;	72E0B2A3115E9D154 CRC64;
Query Match				
Best Local Similarity			11.9%;	Score 72.5; DB 1; Length 262;
Matches	24; Conservative		37.5%;	Fred. No. 4.1; 21; Indels 13; Gaps 4;
QY		39	TWMSNCICRDSGTDSDV	-----DT-----QQQQAENSAVFTADTRSPDRFVRPPRG 87
DB		137	TQNNNV-QQDSQTSKNVPTQDADTKSP	TAQPEQAENSA-PTAEQTSPQLQSAPEKNG 194
QY		88	RGPH 91	
DB		195	TGQH 198	
RESULT 10				
MSA2-FLAP7				
ID	MSA2-FLAP7	STANDARD;	PRT;	272 AA.
AC	P50498;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite			
DE	surface antigen).			
GN	MSA2.			
OS	Plasmodium falciparum (isolate 3D7).			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
NCBI	TaxID=36329;			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=90205972; PubMed=2181307;			
RX	Smythe J.A.; Peterson M.G.; Coppel R.L.; Saul A.J.; Kemp D.J.,			
RA	Anders R.F.;			
RT	"Structural diversity in the 45-kilodalton merozoite surface antigen			
RT	of Plasmodium falciparum."			
RL	Mol. Biochem. Parasitol. 39:227-234 (1990).			
CC	-!- FUNCTION: May play a role in the merozoite attachment to the			
CC	erythrocyte.			
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor			
CC	(Potential).			
CC	-!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; M28991; AAA29686.1; -.			
DR	InterPro; IPR001136; MSA_2.			
DR	PFam; PF00985; MSA_2; 1.			
KW	Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;			
KW	GPI-anchor; Merozoite.			
FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	248	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	249	272	HYDROPHOBIC, REMOVED DURING MATURATION
FT				(BY SIMILARITY).
FT	DOMAIN	44	198	POLYMORPHIC REGION.
FT	DOMAIN	95	108	POLY-THR.

FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 272 AA; 27971 MW; 9D9CF223BF2B483D CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 272;
 Best Local Similarity 37.5%; Pred. No. 4.3;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSSTDSV-----DT-----QOQAENSAVPTADTRSQPRDPVPRRG 87
 DB 147 TQNSNV-QQDSQTKSNVPTQDADTKSPAQPEAENSA-PTAEQTESPELQSAPEKNG 204

QY 88 RGPB 91
 DB 205 TGQH 208

RESULT 11
 MSA2_PLAF6
 ID MSA2_PLAF6 STANDARD; PRT; 274 AA.
 AC P50457;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface antigen 2 precursor (MSA-2).
 GN MSA2.
 OS Plasmodium falciparum (isolate Kf1916).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=57269;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92178286; PubMed=1542312;
 RA Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
 RT "Two novel alleles within subfamilies of the merozoite surface
 antigen 2 (MSA-2) of plasmodium falciparum";
 RL Mol. Biochem. Parasitol. 50:181-184(1992).
 CC -!- FUNCTION: May play a role in the merozoite attachment to the
 erythrocyte.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 (Potential).
 CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 or send an email to license@isb-sib.ch).
 CC EMBL; M73810; AAA29698.1; -;
 CC PIR; A45632; A45632.
 CC InterPro; IPR001136; MSA_2.
 CC Pfam; PF00985; MSA_2; 1.
 CC Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KW GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT CHAIN 21 250
 FT PROPEP 251 274
 FT MEROZOITE SURFACE ANTIGEN 2.
 FT HYDROPHOBIC, REMOVED DURING MATURATION
 FT (BY SIMILARITY).
 FT POLYMORPHIC REGION.
 FT DOMAIN 44 200
 FT DOWIN 97 110
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 274 AA; 28367 MW; CBA832D766F743A2 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 274;
 Best Local Similarity 37.5%; Pred. No. 4.3;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSSTDSV-----DT-----QOQAENSAVPTADTRSQPRDPVPRRG 87
 DB 149 TQNSNV-QQDSQTKSNVPTQDADTKSPAQPEAENSA-PTAEQTESPELQSAPEKNG 206

QY 88 RGPB 91
 DB 207 TGQH 210

RESULT 12
 MSA2_PLAF6
 ID MSA2_PLAF6 STANDARD; PRT; 287 AA.
 AC P19260;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 2)
 DE (Membrane protein PF7).
 GN MSA2.
 OS Plasmodium falciparum (isolate FCR-3 / Gambia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90349616; PubMed=1696728;
 RA Elliott J.F., Allrecht G.R., Gilladoga A., Handunnetti S.M.,
 RA Neequaye J., Lallinger G., Minjas J.N., Howard R.J.;
 RT "Genes for Plasmodium falciparum surface antigens cloned by
 expression in COS cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91117264; PubMed=1990294;
 RA Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
 RA Ridley R., Scaife J.G., McBride J.S.;
 RT "Structural and antigenic polymorphism of the 35- to 48-kilodalton
 merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
 falciparum";
 RL Mol. Cell. Biol. 11:963-971(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91218803; PubMed=2090943;
 RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
 RT "Sequence comparison of allelic forms of the Plasmodium falciparum
 merozoite surface antigen MSA2";
 RL Mol. Biochem. Parasitol. 43:211-220(1990).
 CC -!- FUNCTION: May play a role in the merozoite attachment to the
 erythrocyte.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 (Potential).
 CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 CC EMBL; M28890; AAA29650.1; -;
 CC EMBL; X53832; CAA37829.1; -;
 CC EMBL; M60188; AAA29688.1; -;
 CC PIR; B39615; B39615.
 CC InterPro; IPR001136; MSA_2.
 CC Pfam; PF00985; MSA_2; 1.
 CC Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KW GPI-anchor; Merozoite.
 FT SIGNAL 1
 FT POTENTIAL. 20

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FT CHAIN 21 263 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 264 287 HYDROPHOBIC, REMOVED DURING MATURATION
FT FT (BY SIMILARITY).
FT DOMAIN 44 213 POLYMORPHIC REGION.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 28555 MW; 3968B90DA917AF8 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 287;
Best Local Similarity 37.5%; Pred. No. 4.5;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWMNSICRDSGTDSDV-----DT-----QQQAENSAPVTADTRSPQRPDPVPRRG 87
Db 162 TQNSNV-QQDSQTKSNVPTQADTKSPQAQEAENSA-PTAQTESPELQSAPEKNG 219
QY 88 RGP 91
Db 220 TQGH 223

RESULT 13
MSA2 PLAFI STANDARD; PRT; 300 AA.
AC Q03644;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
MSA2.
GN Plasmodium falciparum (isolate imr143).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57268;
RN [1]
RX MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
antigen 2."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; M59767; AAA29695.1; -.
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT CHAIN 1 20 POTENTIAL.
FT PROPEP 21 276 MEROZOITE SURFACE ANTIGEN 2.
FT FT HYDROPHOBIC, REMOVED DURING MATURATION
FT FT (BY SIMILARITY).
FT DOMAIN 44 226 POLYMORPHIC REGION.
FT SIGNAL 1 20 POLY-THR.
FT CARBOHYD 129 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 28555 MW; 3968B90DA917AF8 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;

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FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30131 MW; A01E17D36075D7D6 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;
Best Local Similarity 37.5%; Pred. No. 4.8;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWMNSICRDSGTDSDV-----DT-----QQQAENSAPVTADTRSPQRPDPVPRRG 87
Db 175 TQNSNV-QQDSQTKSNVPTQADTKSPQAQEAENSA-PTAQTESPELQSAPEKNG 232
QY 88 RGP 91
Db 233 TQGH 236

RESULT 14
MSA2 PLAFZ STANDARD; PRT; 300 AA.
AC Q03645;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate mad71 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70154;
RN [1]
RX MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
antigen 2."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -1- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -1- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; M59768; AAA29696.1; -.
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT CHAIN 1 20 POTENTIAL.
FT PROPEP 21 276 MEROZOITE SURFACE ANTIGEN 2.
FT FT HYDROPHOBIC, REMOVED DURING MATURATION
FT FT (BY SIMILARITY).
FT DOMAIN 44 226 POLYMORPHIC REGION.
FT SIGNAL 1 20 POLY-THR.
FT CARBOHYD 129 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30101 MW; E4116107747AA10D CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:27:15 ; Search time 21 seconds
(without alignments)
535.924 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGWVFLASRLGQGL.....QNVGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85.5	14.0	290	2 T22161	hypothetical prote
2	79	13.0	612	2 T37181	thiamin biosynthes
3	75.5	12.4	900	2 B87957	protein Y1066GD.7
4	75.5	12.4	948	2 T26417	hypothetical prote
5	75	12.3	278	2 S39310	merozoite surface
6	75	12.3	286	2 B45632	merozoite surface
7	73.5	12.1	91	2 PLO227	T-cell receptor be
8	73	12.0	1466	1 CGH07L	collagen alpha 1(I
9	73	12.0	2218	2 B84683	hypothetical prote
10	72.5	11.9	265	2 T05085	hypothetical prote
11	72.5	11.9	272	2 G71618	merozoite surface
12	72.5	11.9	274	2 A45632	merozoite surface
13	72.5	11.9	287	2 B39615	merozoite 45K surf
14	72.5	11.9	300	2 A39112	merozoite 45K surf
15	72.5	11.9	302	2 A39112	merozoite 45K surf
16	72.5	11.9	347	2 B39112	hypothetical prote
17	72.5	11.9	458	2 S24457	hypothetical prote
18	72	11.8	707	2 T26218	hypothetical prote
19	72	11.8	1787	2 T20160	NS3a homolog - mur
20	71.5	11.7	390	2 A47312	hypothetical prote
21	71	11.7	210	2 T41982	transcription regu
22	71	11.7	1479	2 T17401	trithorax protein
23	70.5	11.6	3759	2 A35085	hypothetical prote
24	70	11.5	113	2 T24164	hypothetical prote
25	69.5	11.4	219	2 T19828	hypothetical prote
26	69.5	11.4	318	2 C14851	hypothetical prote
27	69.5	11.4	773	2 F90537	lipoprotein impor
28	69	11.3	261	2 A3070	conserved hypothet
29	69	11.3	281	2 S26052	hypothetical prote

30	69	11.3	319	2 H98216	hypothetical prote
31	69	11.3	545	2 P84533	Mutator-like trans
32	69	11.3	775	2 B72074	hypothetical prote
33	69	11.3	775	2 C81594	hypothetical prote
34	69	11.3	775	2 D86549	hypothetical prote
35	69	11.3	876	2 PC2219	polypeptide - hepa
36	68.5	11.2	361	2 B56940	integral membrane
37	68.5	11.2	788	2 T25061	hypothetical prote
38	68	11.2	85	2 JH0786	transcription fact
39	68	11.2	130	2 B45613	surface antigen FU
40	68	11.2	208	2 T46896	merozoite surface
41	68	11.2	272	2 T29446	hypothetical prote
42	68	11.2	351	2 T51513	hypothetical prote
43	68	11.2	445	2 A56043	steroid hormone re
44	68	11.2	482	2 A70963	hypothetical prote
45	68	11.2	504	2 S75134	cell division prot

ALIGNMENTS

RESULT 1

T22161

hypothetical protein F44D12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22161

R:Coles, L.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19525

A:Accession: T22161

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-290 <WIL>

A:Cross-references: EMBL:Z68298; PIDN:CAA92602.1; GSPDB:GN00022; CESP:F44D12.6

A:Experimental source: clone F44D12

C:Genetic(s):

A:Gene: CESP:F44D12.6

A:Map position: 4

A:Introns: 19/3; 154/2; 198/3

Query Match		14.0%;	Score 85.5;	DB 2;	Length 290;
Best Local Similarity		30.0%;	Pred. No. 0.47;		
Matches		27;	Conservative	15;	Mismatches 31;
				Indels	17;
				Gaps	5;
QY	24	EEHTAHLGTGGAATTGWN-SCICRDSGTD-----DSVDTQQQQAENSAPVADTRSQP	77		
Db	154	DARV-HWRETGLAFIIRSDACRSKDDGGCDTIDSQNSKEDQERSKYNSEMPJSD-----	207		
QY	78	RDVPRPRRGPGPHEPRRKQNVGDLVLT	107		
Db	208	KPDRKQ-----ETPRSKQRTFGPMPT	232		

RESULT 2

T37181

thiamin biosynthesis protein thic SCQ11.11 [similarity] - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000

C:Accession: T37181

R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21598

A:Accession: T37181

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-612 <SEE>

A:Cross-references: EMBL:AL096823; PIDN:CAB46966.1; GSPDB:GN00070; SCQDB:SCQ11.11

A:Experimental source: strain A3(2)

C:Genetic(s):

A:Gene: thic; SCQDB:SCQ11.11

C:Superfamily: thiamin biosynthesis protein thic

Query Match 13.0%; Score 79; DB 2; Length 612;
 Best Local Similarity 31.2%; Pred. No. 4.6;
 Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

QY 39 TMGNSCICRDSG--TDSVDVTDQQA-----ENSAVPTADTRSQPRDPVPR-----83
 DB 60 TNGSVTLYDTSGYTDLVDVTVRGLAPLRNWIARGDTBEYACRPVPRPDDGKHT 119

QY 84 -PRGRG-----PHEPRKKQNVLDGLVDTLAVIR 112
 DB 120 SPRGGLRLNDVAFPRPQPRGRGDGNVQTLAYAR 155

RESULT 3
 B87957
 Protein Y106G6D.7 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: B87957
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: B87957
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-900 <STO>
 A:Cross-references: GB:chr_I; PIDN:CAA20980.1; PID:g3880680; GSPDB:GN000019; CESP:Y106G6D
 C:Genetics:
 A:Gene: Y106G6D.7
 A:Map position: 1

Query Match 12.4%; Score 75.5; DB 2; Length 900;
 Best Local Similarity 31.7%; Pred. No. 16;
 Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

QY 50 SGTDDSVDTQQAENSAVPTADTRSQPRDPVPR-----PPRGRGPHPRKKQ 98
 DB 496 SHEDDDKSRSRWEN-----TSPISRPRSLRDNDRSRSPFRRRRRSRSPRRREE 551

QY 99 NVD 101
 DB 552 HTD 554

RESULT 4
 T26417
 Hypothetical protein Y106G6D.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26417
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z20211
 A:Accession: T26417
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-948 <WIL>
 A:Cross-references: EMBL:AL031629; PIDN:CAA20980.2; GSPDB:GN000019; CESP:Y106G6D.7
 A:Experimental source: clone Y106G6D
 C:Genetics:
 A:Gene: CESP:Y106G6D.7
 A:Map position: 1
 A:Introns: 68/3; 160/3; 270/2; 624/2; 706/3; 888/3; 924/3

Query Match 12.4%; Score 75.5; DB 2; Length 948;
 Best Local Similarity 31.7%; Pred. No. 16;
 Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

QY 50 SGTDDSVDTQQAENSAVPTADTRSQPRDPVPR-----PPRGRGPHPRKKQ 98
 DB 496 SHEDDDKSRSRWEN-----TSPISRPRSLRDNDRSRSPFRRRRRSRSPRRREE 551

DB 544 SHEDDDKSRSRWEN-----TSPISRPRSLRDNDRSRSPFRRRRRSRSPRRREE 599

QY 99 NVD 101
 DB 600 HTD 602

RESULT 5
 S39310
 merozoite surface antigen - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
 C:Accession: S39310
 R:Ramamoji, R.; Ranasinghe, C.
 submitted to the EMBL Data Library, November 1993
 A:Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
 A:Reference number: S39310
 A:Accession: S39310
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-278 <RAM>
 A:Cross-references: EMBL:X76087; NID:9434996; PID:g836639
 C:Superfamily: Epstein-Barr virus nuclear antigen
 C:Keywords: surface antigen

Query Match 12.3%; Score 75; DB 2; Length 278;
 Best Local Similarity 34.6%; Pred. No. 5;
 Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

QY 32 GTGGA-----ATTMGNSCICRDSGTTDSV-----DT-----QQAENSAVPTADT 73
 DB 139 GNGGVQKPNQANKETQNNNV-QQDSQTKSNVPTQADTKSPTAQPEQENSA-PTAEQ 196

QY 74 RSQPRDPVPRPRGRGP 91
 DB 197 TSPFELQSAFENKGTGQH 214

RESULT 6
 B45632
 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C:Accession: B45632
 R:Marshall, V.M.; Coppel, R.L.; Anders, R.P.; Kemp, D.J.
 Mol. Biochem. Parasitol. 50, 181-184, 1992
 A:Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
 A:Reference number: A45632; MUID:92178286; PMID:1542312
 A:Accession: B45632
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <MAR>
 A:Experimental source: isolate 311
 A:Note: sequence extracted from NCBI backbone (NCBI:85255, NCBI:85259)
 C:Superfamily: Epstein-Barr virus nuclear antigen
 C:Keywords: surface antigen

Query Match 12.3%; Score 75; DB 2; Length 286;
 Best Local Similarity 34.6%; Pred. No. 5.1;
 Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

QY 32 GTGGA-----ATTMGNSCICRDSGTTDSV-----DT-----QQAENSAVPTADT 73
 DB 147 GNGGVQKPNQANKETQNNNV-QQDSQTKSNVPTQADTKSPTAQPEQENSA-PTAEQ 204

QY 74 RSQPRDPVPRPRGRGP 91
 DB 205 TSPFELQSAFENKGTGQH 222

RESULT 7
 PL0227
 T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 30-May-1997
 C;Accession: P0227
 R;Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Posnett, D.N.
 J. Exp. Med. 171, 221-230, 1990
 A;Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.
 A;Reference number: P0225; MUID:9011615; PMID:1967299
 A;Accession: P0227
 A;Molecule type: mRNA
 A;Residues: 1-91 <LIV>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 12.1%; Score 73.5; DB 2; Length 91;
 Best Local Similarity 34.1%; Pred. No. 2.1;
 Matches 30; Conservative 8; Mismatches 21; Indels 29; Gaps 5;

Qy 7 AVFLASSLGGGLLTLEHIAHFLGTAATMGNSICRDPDSG-----TDDSV 56
 Db 10 ALVYRQSLGGL-----EFLVY-----QGNS--APDXSLPDRFSAERTGGSV 53

Qy 57 DT---QQQAENSAVPTADTRSPRPDV 81
 Db 54 STLTIQRTQEDSAVYLCAAMPVPRDPV 81

RESULT 8
 CGHUTL
 collagen alpha 1(III) chain precursor - human
 N;Alternate names: procollagen alpha 1(III) chain
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C;Accession: S05272; S04642; P0011; S01726; S04887; A90399; A94562; I51868; S59511; A90399
 R;Prockop, D.J.
 submitted to the EMBL Data Library, February 1989
 A;Reference number: S05272
 A;Accession: S05272
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1240, 'V', 1242-1466 <PRC>
 A;Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
 R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
 Biochem. J. 260, 509-516, 1989
 A;Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of human
 erences.
 A;Reference number: S04642; MUID:89350838; PMID:2764886
 A;Accession: S04642
 A;Molecule type: mRNA
 A;Residues: 1-1196 <ALA>
 A;Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
 A;Note: the complete sequence is not shown
 R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
 Gene 78, 255-265, 1989
 A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
 A;Reference number: P0011; MUID:89378752; PMID:2777083
 A;Accession: P0011
 A;Molecule type: DNA
 A;Residues: 1-176 <BEN>
 A;Cross-references: GB:M26939; NID:G180813; PIDN:AAA52040.1; PID:G180814
 R;Tomam, P.D.; Ricca, G.A.; de Crombrughe, B.
 Nucleic Acids Res. 16, 7201, 1988
 A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre
 A;Reference number: S01726; MUID:88303360; PMID:3405773
 A;Accession: S01726
 A;Molecule type: mRNA
 A;Residues: 1-170 <TOM>
 A;Cross-references: EMBL:X07240; NID:G30060; PIDN:CAA30229.1; PID:G30061
 A;Note: the authors translated the codon CAG for residue 154 as His
 R;Janeczko, R.A.; Ramirez, F.
 Nucleic Acids Res. 17, 6742, 1989
 A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
 A;Reference number: S04887; MUID:89386015; PMID:2780304
 A;Accession: S04887

A;Molecule type: mRNA
 A;Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634, '
 A;Cross-references: EMBL:X15332; NID:G29545; PIDN:CAA33387.1; PID:G930045
 A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 16, 1158-1164, 1977
 A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides
 A;Reference number: A90399; MUID:77134724; PMID:557335
 A;Accession: A90399
 A;Molecule type: protein
 A;Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294, 'S', 296-398 <SEY1>
 A;Experimental source: liver
 A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose
 R;Seyer, J.M.
 submitted to the Atlas, December 1977
 A;Reference number: A94562
 A;Accession: A94562
 A;Molecule type: protein
 A;Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY2>
 A;Experimental source: liver
 A;Note: author submitted corrections to A90399
 R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
 Am. J. Hum. Genet. 53, 62-70, 1993
 A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
 splicing.
 A;Reference number: I51868; MUID:93304430; PMID:8317500
 A;Accession: I51868
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 186-194 <ML>
 A;Cross-references: GB:S62925; NID:G386425; PIDN:AAD13937.1; PID:G4261637
 R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
 Biochem. J. 311, 939-943, 1995
 A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3A
 A;Reference number: S59511; MUID:96067614; PMID:7487954
 A;Accession: S59511
 A;Molecule type: mRNA
 A;Residues: 302-423 <CHI>
 A;Cross-references: GB:S79877; NID:G1195576; PIDN:AAAB35615.1; PID:G1195577
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 17, 3404-3411, 1978
 A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe
 A;Reference number: A90414; MUID:79000343; PMID:687591
 A;Accession: A90414
 A;Molecule type: protein
 A;Residues: 399-675, 'N', 677-727 <SEY3>
 A;Experimental source: liver
 R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
 J. Biol. Chem. 266, 5256-5259, 1991
 A;Title: G to T transversion at position +5 of a splice donor site causes skipping of the
 A;Reference number: I55349; MUID:91161621; PMID:1672129
 A;Accession: I55349
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 537-605 <LEE>
 A;Cross-references: GB:M59312; NID:G180815; PIDN:AAA52041.1; PID:G180816
 R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
 Biochemistry 19, 1583-1589, 1980
 A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty
 A;Reference number: A90438; MUID:80198282; PMID:6246925
 A;Accession: A90438
 A;Molecule type: protein
 A;Residues: 728-895, 'A', 897-964 <SEY4>
 A;Experimental source: liver
 R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan,
 J. Biol. Chem. 265, 17070-17077, 1990
 A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping and
 A;Reference number: A38303; MUID:91009133; PMID:2145268
 A;Accession: A38303
 A;Molecule type: mRNA
 A;Residues: 861-1015 <COL>
 A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:G180878; PIDN:AAAB59383.1; PID:G3
 A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos synd

R;Mankoo, B.S.; Dalglish, R.
 Nucleic Acids Res. 16, 2337, 1988
 A>Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
 A;Reference number: S02119; MUID:8818927; PMID:3357782
 A;Accession: S02119
 A>Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
 A;Cross-references: EMBL:X06700; NID:G30053; PIDN:CAA29886.1; PID:G30054
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 20, 2621-2627, 1981
 A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
 A;Reference number: A90446; MUID:81208139; PMID:7016180
 A;Accession: A90446
 A;Molecule type: protein
 A;Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-
 A;Experimental source: liver
 R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
 Nucleic Acids Res. 12, 9393-9394, 1984
 A>Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
 A;Reference number: A93551; MUID:85087944; PMID:6096827
 A;Accession: A93551
 A;Molecule type: mRNA
 A;Residues: 1065-1155, 'P', 1157-1466 <LOI>
 A;Cross-references: EMBL:X01655; EMBL:X01742; NID:G29584; PIDN:CAA25821.1
 R;Miskulin, M.; Dalglish, R.; Kluge-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brand
 Biochemistry 25, 1408-1413, 1986
 A>Title: Human type III collagen gene expression is coordinately modulated with the type
 A;Reference number: I52393; MUID:86187804; PMID:3754462
 A;Accession: I52393
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1161-1200 <MIS>
 A;Cross-references: GB:M11146; NID:G180415; PIDN:AAA52003.1; PID:G180416
 R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
 A>Title: Human alpha 1(III) and alpha 2(IV) procollagen genes are located on the long arm
 A;Reference number: I59025; MUID:85216505; PMID:3858926
 A;Accession: I79359
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1165-1196 <EMA>
 A;Cross-references: GB:M11134; NID:G180417; PIDN:AAA52004.1; PID:G180418
 R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
 J. Biol. Chem. 260, 4357-4363, 1985
 A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen.
 A;Reference number: A92516; MUID:85157600; PMID:2579949
 A;Accession: A92516
 A;Molecule type: DNA
 A;Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>
 A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
 A;Experimental source: liver
 A;Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given
 A;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
 C;Genetics:
 A;Gene: GDB:COL3A1
 A;Cross-references: GDB:118729; OMIM:120180
 A;Map position: 2q31-2q31
 A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
 A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
 C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide
 er of their length, is formed with desmosine cross-links made from lysine and allysine
 C;Function:
 A;Description: structural component of extracellular fibrous polymer that maintains inte
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-153/Domain: amino-terminal propeptide #status predicted <PRO>
 F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
 F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
 F;154-167/Region: amino-terminal nonhelical telopeptide

F;168-1196/Region: cell attachment (R-G-D) motif
 F;1091-1093/Region: carboxyl-terminal nonhelical telopeptide
 F;1197-1221/Region: carboxyl-terminal propeptide #status predicted <CPR>
 F;1222-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
 F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
 F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
 F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F;161-1212/Modified site: allysine (Lys) #status predicted
 F;263-1284, 860, 977, 1106/Modified site: 5-hydroxylysine (Lys) #status experimental
 F;263/Binding site: carboxylate (Lys) (covalent) #status experimental
 F;584-1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
 F;948-949/Cleavage site: Gly-Asp (collagenase) #status experimental
 F;1106/Binding site: carboxylate (Lys) (covalent) #status predicted
 Query Match 12.0%; Score 73; DB 1; Length 1466;
 Best Local Similarity 28.8%; Pred. No. 47;
 Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;
 QY 16 GQGLLTLEH---IAHFLGTGGAATTMGNS-----CICRDSGT---DPS 55
 DB 8 GSWLLALLHPITILAAQAEVGGCHLGSYADRDVWKEPCQICVC--DSGSLCDDI 65
 QY 56 V-DTQQQAEASAVP-----TATRSQPRDPVPRGRGPHPR 94
 DB 66 ICDDQLDCPNPEIPFGECACVCPQPTATPRPP-NGQPGQGP 108
 RESULT 9
 B84683
 hypothetical protein At2g29300 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: B84683
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84683
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2218 <STO>
 A;Cross-references: GB:AE002093; NID:G4803953; PIDN:AAD29825.1; GSPDN:GN00139
 C;Genetics:
 A;Gene: At2g28300
 A;Map position: 2
 Query Match 12.0%; Score 73; DB 2; Length 2218;
 Best Local Similarity 29.9%; Pred. No. 73;
 Matches 29; Conservative 17; Mismatches 19; Indels 32; Gaps 7;
 QY 45 ICRDSS-----GRDSSV--DTQQQAEASA---VPTADTRS---QPRDPVPRP--- 84
 DB 49 LCQTESPDSPQKGGEGSERSLANDTSNIPVENSSTLLPTSTQATVQPMPEVRPQSHT 108
 QY 85 -----RGRGPHPRKKQNVGLVLTAVIRT 113
 DB 109 LKETOPIKRGK--RFXRTDKALTPVSL--AVSRT 141
 RESULT 10
 T05085
 hypothetical protein T6K21.170 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C;Accession: T05085
 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Bancroft, I.; Mewes, I.
 submitted to the Protein Sequence Database, February 1998
 A;Reference number: 215397
 A;Accession: T05085
 A;Molecule type: DNA

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A;Residues: 1-265 <BEV>
A;Cross-references: EMBL:AL021889
A;Experimental source: cultivar Columbia; BAC clone T6K21
C;Genetics:
A;Map position: 4
A;Introns: 37/3; 59/2; 93/3; 163/1; 192/1
A;Note: T6K21.170

Query Match      11.9%; Score 72.5; DB 2; Length 265;
Best Local Similarity 37.5%; Pred. No. 8.4;
Matches 36; Conservative 24; Mismatches 38; Indels 55; Gaps 9;

QY 2 IVFGWAVFLASR--SIQQGLLLLEBIAH-----FLG-----TGGAA 37
DB 112 VCIGYITLVAKOPSAG--GSLVTFQTKVHEDYSKINTLVYIARLKSQPPDPBEIGGAK 170

QY 38 TTWNS-----CICKDDSGTDSVDTQOQAENSAPVTADTRSPRPV-----RPPRRG 87
DB 171 TGLGSSILGTCIHPCKSVSKSVETEN-----VKQPNELKARNVFIIRVYYPNKG 224

QY 88 RGP-----HEPRRKQNVGLVLTFLAVIRTLVD 116
DB 225 RAPKNGHKKPR-----DRAIIKRTMD 247

RESULT 11
merozoite surface antigen MSP-2 PFB0300C - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 17-Nov-2000
C;Accession: G71618; A44950
R;Gardner, M.J.; Tetzelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
R;Peretea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-272 <GAR>
A;Cross-references: GB:AF001385; GB:AE001362; NID:g3845143; PIDN:AAC71849.1; PID:g384514
A;Experimental source: clone 3D7
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: A44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54, 'T', 56-272 <SMY>
A;Cross-references: GB:M28891; NID:g160458; PID:g160459
C;Genetics:
A;Gene: PFB0300C
A;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

Query Match      11.9%; Score 72.5; DB 2; Length 272;
Best Local Similarity 37.5%; Pred. No. 8.6;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWGNSICTRDSGTDSV-----DT-----QQQAENSAPVTADTRSQPRDPVPPRRG 87
DB 147 TQNNSNV-QQDSQTKSNVPTQDADTKSPTAQPEQAENSA-PTAEQTSPESLOAPENKNG 204

QY 88 RGP 91
DB 205 TGOH 208

RESULT 12
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 17-Nov-2000
C;Accession: A45632
R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Contents: KFI916
A;Accession: A45632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <MAR>
A;Cross-references: GB:M73810; NID:g160484; PID:g160485
A;Note: sequence extracted from NCBI backbone (NCBI:85252, NCBIP:85257)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

Query Match      11.9%; Score 72.5; DB 2; Length 274;
Best Local Similarity 37.5%; Pred. No. 8.7;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWGNSICTRDSGTDSV-----DT-----QQQAENSAPVTADTRSQPRDPVPPRRG 87
DB 149 TQNNSNV-QQDSQTKSNVPTQDADTKSPTAQPEQAENSA-PTAEQTSPESLOAPENKNG 206

QY 88 RGP 91
DB 207 TGOH 210

RESULT 13
merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: membrane antigen pf7
C;Species: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 01-Dec-2000
C;Accession: B39615; A36018; B44950; A45613
R;Penton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaife
Mol. Cell. Biol. 11, 963-971, 1991
A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
A;Reference number: A39615; MUID:91117264; PMID:1990294
A;Accession: B39615
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <FEN>
A;Cross-references: EMBL:X53833
A;Note: clone T9-94
R;Elliot, J.F.; Albrecht, G.R.; Gilladoga, A.; Handunnetti, S.M.; Neequaye, J.; Lallings
Proc. Natl. Acad. Sci. U.S.A. 87, 6363-6367, 1990
A;Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS cel
A;Reference number: A36018; MUID:90349616; PMID:1696728
A;Accession: A36018
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <ELL>
A;Cross-references: GB:M28890; NID:g160406; PID:g160407
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: B44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186, 'R', 188-287 <SMY>
A;Cross-references: GB:M28892; NID:g160488; PID:g160489
R;Fandeur, T.; Bonnefoy, S.; Mercereau-Puijalon, O.
Mol. Biochem. Parasitol. 47, 167-178, 1991
A;Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are genet
A;Reference number: A45613; MUID:92049549; PMID:1944415
A;Accession: A45613
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 28, 'E', 30-186, 'R', 188-230, 'IH' <FAN>
A;Experimental source: Uganda Palo Alto strain, merozoite

```

A;Note: sequence extracted from NCBI backbone (NCBIP:65035)
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: membrane protein; surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 287;
 Best Local Similarity 37.5%; Pred. No. 9.1; Indels 13; Gaps 4;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;
 QY 39 TMGNSICRDSGTDSDV-----DT-----QQQAENSAPVPTADTRSPQRPDPVPPRRG 87
 DB 162 TQNSNV-QQDSQTSKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPPELQSAPEKNG 219
 QY 88 RGPH 91
 DB 220 TGOH 223

RESULT 14

A39112
 merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (isol
 C;Species: Plasmodium falciparum
 C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
 C;Accession: A39112
 R;Smythe, J.A.; Coppal, R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; Ander
 Proc. Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991
 A;Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.
 A;Reference number: A39112; MUID:91156685; PMID:2000383
 A;Accession: A39112
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-300 <SMY>
 A;Cross-references: GB:M59765
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 300;
 Best Local Similarity 37.5%; Pred. No. 9.5;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSICRDSGTDSDV-----DT-----QQQAENSAPVPTADTRSPQRPDPVPPRRG 87
 DB 175 TQNSNV-QQDSQTSKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPPELQSAPEKNG 232
 QY 88 RGPH 91
 DB 233 TGOH 236

RESULT 15

A39615
 merozoite 45K surface antigen precursor (clone T9-96) - malaria parasite (Plasmodium fal
 C;Species: Plasmodium falciparum
 C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 17-Nov-2000
 C;Accession: A39615; S13802
 R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaif
 Mol. Cell. Biol. 11, 963-971, 1991
 A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
 A;Reference number: A39615; MUID:91117264; PMID:1990294
 A;Accession: A39615
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-302 <FEN>
 A;Cross-references: EMBL:X53832
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 302;
 Best Local Similarity 37.5%; Pred. No. 9.6;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSICRDSGTDSDV-----DT-----QQQAENSAPVPTADTRSPQRPDPVPPRRG 87
 DB 177 TQNSNV-QQDSQTSKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPPELQSAPEKNG 234

QY 88 RGPH 91
 DB 235 TGOH 238

Search completed: April 2, 2004, 10:31:06
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:25:15 ; Search time 54 Seconds
(without alignments)
612.186 Million cell updates/sec

Title: US-10-002-796-9
Perfect score: 609
Sequence: 1 MIYFGWAVFLASRLGQLL.....QNVDELVLTLAVIRLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	609	100.0	117	4	AAB31180 Amino aci
2	609	100.0	117	6	ABO25151 Novel hum
3	609	100.0	117	6	ABU67269 Novel hum
4	609	100.0	117	6	ABU72037 Novel hum
5	609	100.0	117	6	ABU67138 Novel hum
6	609	100.0	117	6	ABU79780 Human sec
7	609	100.0	117	6	ABO33583 Novel hum
8	609	100.0	117	6	ADA47181 Human sec
9	609	100.0	117	7	ABO44436 Human sec
10	609	100.0	117	7	ABO33460 Novel hum
11	609	100.0	117	7	ABO19838 Human sec
12	609	100.0	117	7	ADC17875 Human PRO
13	609	100.0	117	7	ADD10295 Human sec
14	609	100.0	117	7	ADD11255 Human sec
15	609	100.0	117	7	ADD70521 Human sec
16	609	100.0	117	7	ADD39598 Human sec
17	609	100.0	117	7	ADD70044 Human sec
18	609	100.0	117	7	ADD37048 Human sec
19	609	100.0	117	7	ADD38165 Human sec
20	609	100.0	117	7	ADD39121 Human sec
21	609	100.0	117	7	ADD38644 Human sec
22	609	100.0	117	7	ADD40075 Human sec
23	609	100.0	117	7	ADE50296 Human sec
24	609	100.0	117	7	ADE19908 Human sec
25	609	100.0	117	7	ADE49819 Human sec

26	609	100.0	117	7	ADE21377 Human sec
27	609	100.0	117	8	ADE41256 Human sec
28	609	100.0	117	8	ADE41104 Human sec
29	609	100.0	118	3	AAY99341 Human PRO
30	609	100.0	118	4	AAB66090 Protein O
31	609	100.0	118	5	ABB84819 Human PRO
32	609	100.0	118	5	ABB95425 Human ang
33	604	99.2	289	4	AAW25871 Human PRO
34	604	99.2	427	2	AAW25761 Human sec
35	604	99.2	427	3	AAB32412 Human sec
36	604	99.2	436	3	AAB32411 Human sec
37	604	99.2	576	3	AAB32384 Human sec
38	604	99.2	576	4	AAB94297 Human PRO
39	604	99.2	576	5	ABP64599 Human PRO
40	85	14.0	361	6	ABU21450 Protein O
41	79.5	13.1	5002	4	ABW53723 Drosophila
42	78	12.8	1527	2	AAW81172 Human BAZ
43	78	12.8	1531	2	AAW81173 Human BAZ
44	77	12.6	2618	4	ABG02135 Novel hum
45	77	12.6	2622	4	ABG06418 Novel hum

ALIGNMENTS

RESULT 1
AAB31180
ID AAB31180 standard; protein; 117 AA.
XX
AC AAB31180;
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO444.

XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO242; PRO288; PRO365; PRO361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..16
FT	/note= "signal peptide"
FT	Modified-site 18..24
FT	/note= "N-myristoylation site"
FT	Modified-site 32..38
FT	/note= "N-myristoylation site"
FT	Modified-site 34..40
FT	/note= "N-myristoylation site"
FT	Modified-site 35..41
FT	/note= "N-myristoylation site"
FT	Modified-site 51..57
FT	/note= "N-myristoylation site"
XX	WO200077037-A2.
XX	21-DEC-2000.
XX	22-MAY-2000; 2000WO-US014042.
XX	15-JUN-1999; 99US-0139695P.
XX	20-JUL-1999; 99US-0145070P.
XX	26-JUL-1999; 99US-0145698P.
XX	17-AUG-1999; 99US-0149396P.
XX	01-SEP-1999; 99WO-US020111.
XX	08-SEP-1999; 99WO-US020594.
XX	15-SEP-1999; 99WO-US021090.
XX	15-SEP-1999; 99WO-US021547.
XX	30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-01694959.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
 PI Godowski P, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2001-050091/06.
 DR N-PSDB; AAC86965.
 XX
 PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides.
 XX
 PS Claim 12, Fig 4; 244pp; English.
 XX
 CC The present sequence represents a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO1710,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO333, PRO301, PRO187,
 CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding these
 CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene
 XX
 SQ Sequence 117 AA;

 Query Match 100.0%; Score 509; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MIVFGWAVFLASRLGQGLLLTLESHIAFLGTGGAATTMGNSICRDDSSTGDSVDTQQ 60
 Db 1 MIVFGWAVFLASRLGQGLLLTLESHIAFLGTGGAATTMGNSICRDDSSTGDSVDTQQ 60

 QY 61 QOASNAVPTATRSQPRDPVPPRRGRGPHEPRKKNQVGLVLDTLAVIRTLVXK 117
 Db 61 QOASNAVPTATRSQPRDPVPPRRGRGPHEPRKKNQVGLVLDTLAVIRTLVXK 117

 RESULT 2
 ABO25151
 ID ABO25151 standard; protein; 117 AA.
 XX
 AC ABO25151;
 XX
 DT 05-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX

KW Human, secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal disorder;
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth.
 XX
 OS Homo sapiens.
 XX
 PN US2003040014-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066269.
 PF
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 03-FEB-1998; 98US-0074092P.
 PR 23-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098601P.
 PR 10-SEP-1998; 98US-0098803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019093.
 PR 17-SEP-1998; 98WO-US019130.
 PR 17-SEP-1998; 98US-0100588P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.

KW Human, secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal disorder;
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth.
 XX
 OS Homo sapiens.
 XX
 PN US2003040014-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066269.
 PF
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 03-FEB-1998; 98US-0074092P.
 PR 23-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098601P.
 PR 10-SEP-1998; 98US-0098803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019093.
 PR 17-SEP-1998; 98WO-US019130.
 PR 17-SEP-1998; 98US-0100588P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.

PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2003-503396/47.
 DR N-PSDB; ACD42316.
 XX
 XX
 PT New secreted and transmembrane PRO polypeptides, useful for treating
 PT diabetes, retinal disorders and stimulating an immune response.
 XX
 PS Claim 12; Fig 4; 25app; English.
 XX
 CC The invention describes an isolated polypeptide (I) having at least 80 %
 CC amino acid sequence identity to 30 secreted and transmembrane
 CC polypeptides. PRO polypeptides are also useful for stimulating
 CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
 CC factor stimulated proliferation of endothelial cells, stimulating
 CC proliferation of stimulated T-lymphocytes and for inducing proliferation
 CC of PD12 pancreatic ductal cells and are thus useful in the treatment of
 CC disorders which involve protein secretion by the pancreas, including
 CC diabetes. PRO polypeptides are useful for inducing vascular permeability
 CC and in enhancing survival of retinal neurons cells and are thus useful
 CC for the treatment of retinal disorders. PRO polypeptides are also useful
 CC for stimulating an immune response and inducing inflammation by inducing
 CC mononuclear cell and eosinophil infiltration at the site of infection of
 CC an animal. The PRO polypeptides are further useful for inducing apoptosis
 CC in endothelial cells for inhibiting neoplastic growth. This is the amino
 CC acid sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRLSGQLLLTLEHIAHFTGCGAATTGNSICICRDSGTDSDVDTQ 60
 DB 1 MIVFGWAVFLASRLSGQLLLTLEHIAHFTGCGAATTGNSICICRDSGTDSDVDTQ 60
 QY 61 QOANSAVPTADTRSQPRDPVPRGRGPHPRKQKQNDGLVLTAVIRTLVDK 117
 DB 61 QOANSAVPTADTRSQPRDPVPRGRGPHPRKQKQNDGLVLTAVIRTLVDK 117
 RESULT 3
 ABU67269
 ID ABU67269 standard; protein; 117 AA.
 XX
 AC ABU67269;
 XX

DT 28-MAY-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO444.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO285; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX
 XX Homo sapiens.
 XX
 PN US2003032063-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066494.
 XX
 XX 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062818P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0075294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098601P.
 PR 10-SEP-1998; 98US-0098803P.
 PR 10-SEP-1998; 98US-0098811P.
 PR 14-SEP-1998; 98US-0099812P.
 PR 16-SEP-1998; 98US-0099812P.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98US-0100858P.
 PR 24-SEP-1998; 98US-0101923P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 25-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98US-0109304P.
 PR 08-MAR-1999; 98US-0109304P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 02-JUN-1999; 98US-0125778P.
 PR 15-JUN-1999; 98US-0139695P.
 PR 20-JUL-1999; 98US-0145070P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 17-AUG-1999; 98US-0149396P.
 PR 01-SEP-1999; 98US-02020111.
 PR 08-SEP-1999; 98US-02020111.
 PR 15-SEP-1999; 98US-02020111.
 PR 15-SEP-1999; 98US-02020111.
 PR 30-NOV-1999; 98US-02020111.
 PR 01-DEC-1999; 98US-02020111.
 PR 02-DEC-1999; 98US-02020111.
 PR 07-DEC-1999; 98US-0169495P.
 PR 20-DEC-1999; 98US-0203099P.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005641.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341964/32.
 DR NP-PSDB; ACA04925.
 XX
 PT Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
 PT polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping.
 XX
 XX Claim 12; Fig 4; 255pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO377, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO4630, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (ii) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (i) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (ii) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This is the amino acid
 CC sequence of a novel human secreted and transmembrane polypeptide
 CC associated oligonucleotide
 XX
 XX Sequence 117 AA;
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRLGGGLLLEHIAHFLGTGGAATMGNSICRDSDGSDVDVQ 60
 Db 1 MIVFGWAVFLASRLGGGLLLEHIAHFLGTGGAATMGNSICRDSDGSDVDVQ 60

QY 61 QQAENSAVPTADTRSQRPDRPVRPRGRGPHPRRKQNVDTGLVDTLAVIRTLVDK 117
 Db 61 QQAENSAVPTADTRSQRPDRPVRPRGRGPHPRRKQNVDTGLVDTLAVIRTLVDK 117
 RESULT 4
 ABU72037
 ID ABU72037 standard; protein; 117 AA.
 XX
 AC ABU72037;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Human; secreted and transmembrane polypeptide; PRO;
 KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2002177165-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 01-FEB-2002; 2002US-00065500.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0085398P.
 PR 18-AUG-1998; 98US-0087000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US023278.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021056.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001WO-US002796.

(GETH) GENENTECH INC.

PI Aehkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-328482/31.
 DR N-PSDB; ACA60455.

FT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 4; 25app; English.

CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO141,
 CC PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
 CC (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
 CC PRO551 polypeptide, and for linking a bioactive molecule to a cell
 CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This is the amino acid
 XX sequence of a novel human secreted and transmembrane PRO polypeptide
 SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDSVDTQQ 60
 DB 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDSVDTQQ 60
 QY 61 QOAEASVPTADTRSQPRDPVPRRGPGHPHPRKKNQVGLVLDTLAVIRTLVDK 117
 DB 61 QOAEASVPTADTRSQPRDPVPRRGPGHPHPRKKNQVGLVLDTLAVIRTLVDK 117
 RESULT 5
 ABU67138
 ID ABU67138 standard; protein; 117 AA.
 XX
 AC ABU67138;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003032062-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066273.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063323P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095988P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0096011P.
 PR 10-SEP-1998; 98US-0098033P.
 PR 10-SEP-1998; 98US-0098811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.

25-NOV-1998; 98WO-US025190.
 01-DEC-1998; 98WO-US025108.
 08-MAR-1999; 98WO-US005028.
 23-MAR-1999; 99US-0125778P.
 02-JUN-1999; 99WO-US012252.
 15-JUN-1999; 99US-0139695P.
 20-JUL-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028565.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 15-NOV-2001; 2001US-00002796.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM;
 Wood WI, Zhang Z;
 WPI; 2003-341963/32.
 N-PSDB; ACA04445.
 New secreted and transmembrane polypeptide for modulating biological
 activity of a cell expressing the polypeptide, identifying agonists or
 antagonists of the polypeptide, and as molecular weight markers.
 Claim 12; Fig 4; 254pp; English.
 The invention describes an isolated, secreted and transmembrane
 polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 PRO333, PRO301, PRO187, PRO337, PRO1411, PRO1096, PRO246, PRO6307,
 PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 cell expressing the polypeptides. The bioactive molecule causes cell
 death. (ii) is useful as hybridisation probes, in chromosome and gene
 mapping, in generation of antisense RNA and DNA, in the preparation of
 PRO polypeptide, for generating transgenic animals or knockout animals
 which in turn are useful in the development and screening of
 therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (i) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (ii) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This is the amino acid
 CC sequence of a novel human secreted and transmembrane polypeptide
 XX Sequence 117 AA;
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63; 0; Indels 0; Gaps 0;
 Matches 117; Conservative 0; Mismatches 0;
 Qy 1 MIVFGMAVFLASRLGQGLLLTLEHIAHFLGTGGAATTGNSCICRDSGTDSDVDTQ 60
 Db 1 MIVFGMAVFLASRLGQGLLLTLEHIAHFLGTGGAATTGNSCICRDSGTDSDVDTQ 60
 Qy 61 QQAENSAVPTADTRSPDRPVRPRGRGPHPRKKQNVGLVLTAVIRTLVDR 117
 Db 61 QQAENSAVPTADTRSPDRPVRPRGRGPHPRKKQNVGLVLTAVIRTLVDR 117
 RESULT 6
 ABU79780
 ID ABU79780 standard; protein; 117 AA.
 XX AC ABU79780;
 XX DT 19-JUN-2003 (first entry)
 XX DE Human secreted/transmembrane protein PRO444.
 XX KW Human; secreted protein; transmembrane protein; PRO; genetic disorder;
 XX gene therapy.
 XX OS Homo sapiens.
 XX US2003032057-A1.
 XX 13-FEB-2003.
 XX 15-NOV-2001; 2001US-00002796.
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 19-SEP-1997; 97US-0059588P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 24-OCT-1997; 97US-0063082P.
 XX 27-OCT-1997; 97US-0063329P.
 XX 29-OCT-1997; 97US-0063733P.
 XX 21-NOV-1997; 97US-0066364P.
 XX 25-NOV-1997; 97US-0066840P.
 XX 16-DEC-1997; 97US-0069694P.
 XX 09-FEB-1998; 98US-0074086P.
 XX 09-FEB-1998; 98US-0074092P.
 XX 25-MAR-1998; 98US-0079294P.
 XX 08-APR-1998; 98US-0081049P.
 XX 14-JUL-1998; 98WO-US014552.
 XX 18-AUG-1998; 98US-0093988P.
 XX 18-AUG-1998; 98US-0097000P.
 XX 09-SEP-1998; 98US-0099601P.
 XX 10-SEP-1998; 98US-0099803P.
 XX 10-SEP-1998; 98US-0099811P.
 XX 10-SEP-1998; 98US-0099812P.
 XX 10-SEP-1998; 98WO-US018824.
 XX 14-SEP-1998; 98WO-US019093.
 XX 16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98US-0100858P.
 17-SEP-1998; 98WO-US019437.
 24-SEP-1998; 98US-0101922P.
 28-OCT-1998; 98US-0106032P.
 28-NOV-1998; 98US-0109304P.
 20-NOV-1998; 98WO-US024855.
 25-NOV-1998; 98WO-US025190.
 01-DEC-1998; 98WO-US025108.
 08-MAR-1999; 99WO-US005028.
 23-MAR-1999; 99US-0125778P.
 12-JUN-1999; 99WO-US012252.
 15-JUN-1999; 99US-0139695P.
 20-JUL-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028365.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032878.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy WA, Stewart TA, Tamas D, Watanabe CK, Williams PM;
 Wood WI, Zhang Z;
 WPI; 2003-341960/32.
 N-PSDB; ACA65586.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 4; 25pp; English.

The invention relates to an isolated, secreted/transmembrane polypeptide, termed PRO polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 37 sequences appearing as ABU79779 -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited under any one of the ATCC numbers given in the specification. Also included are an isolated nucleic acid molecule having at least 80% sequence identity to a sequence selected from any one of the 37 cDNA

sequences defined in the specification (or encoding the mature PRO protein or a PRO protein extracellular domain), a PRO expression vector, a host cell comprising the vector, PRO fusion proteins, anti-PRO antibodies and a method for linking a bioactive molecule to a cell expressing the above PRO polypeptides, the bioactive molecule is a toxin, radiolabel or an antibody and causes the death of the cell. PRO or the antibody is useful for modulating at least one biological activity of cell expressing the above polypeptides. PRO is useful for identifying agonists or antagonists of PRO, for preparing a variant of PRO, as molecular weight markers for protein electrophoresis purpose and PRO nucleic acid is useful for recombinantly expressing those markers. PRO is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. PRO nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, in gene therapy, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes the PRO and for the genetic analysis of individuals with genetic disorders, for chromosome identification, as a chromosome marker, and for generating probes for polymerase chain reaction (PCR), Northern analysis, Southern analysis and Western analysis. The antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, for affinity purification of PRO from recombinant cell culture or natural sources. PRO or Ab is useful for the preparation of medicament for treating conditions which is responsive to the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The present sequence encodes a PRO polypeptide

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLSGQLLTLESHIAHFLGTGAATMGNSICRDDSGTDDSDVDTQQ 60
 DB 1 MIVFGWAVFLASRLSGQLLTLESHIAHFLGTGAATMGNSICRDDSGTDDSDVDTQQ 60
 QY 61 QQAENSAPVTADTRSQPRDPVPPRGRGPHPRKKNQVDGLVLDLTLAVRTLVDK 117
 DB 61 QQAENSAPVTADTRSQPRDPVPPRGRGPHPRKKNQVDGLVLDLTLAVRTLVDK 117

RESULT 7
 ABO33583
 ID ABO33583 standard; protein; 117 AA.
 XX ABO33583;
 AC ABO33583;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; cellac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003073130-A1.
 XX
 XX 17-APR-2003.
 PD
 XX

PF	11-DEC-2001;	2001US-00015869.	
XX			
PR	01-SEP-1998;	98US-0098716P.	98US-0103633P.
PR	01-SEP-1998;	98US-0098723P.	98US-0103678P.
PR	01-SEP-1998;	98US-0098749P.	98US-0103679P.
PR	01-SEP-1998;	98US-0098750P.	98US-0103711P.
PR	01-SEP-1998;	98US-0098803P.	98US-0104257P.
PR	02-SEP-1998;	98US-0098821P.	98US-0104987P.
PR	02-SEP-1998;	98US-0098843P.	98US-0105000P.
PR	09-SEP-1998;	98US-0098936P.	98US-0105002P.
PR	09-SEP-1998;	98US-0098958P.	98US-0105104P.
PR	09-SEP-1998;	98US-0098959P.	98US-0105169P.
PR	09-SEP-1998;	98US-0098960P.	98US-0105266P.
PR	09-SEP-1998;	98US-0098964P.	98US-0105693P.
PR	10-SEP-1998;	98US-0098971P.	98US-0105807P.
PR	10-SEP-1998;	98US-00989754P.	98US-0105881P.
PR	10-SEP-1998;	98US-00989763P.	98US-0105882P.
PR	10-SEP-1998;	98US-00989792P.	98US-0106062P.
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PR	10-SEP-1998;	98US-00989812P.	98US-0106029P.
PR	10-SEP-1998;	98US-00989815P.	98US-0106030P.
PR	10-SEP-1998;	98US-00989816P.	98US-0106032P.
PR	15-SEP-1998;	98US-0100388P.	98US-0106033P.
PR	15-SEP-1998;	98US-0100390P.	98US-0106178P.
PR	15-SEP-1998;	98US-0100398P.	98US-0106248P.
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PR	16-SEP-1998;	98US-0100661P.	98US-0106500P.
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PR	18-SEP-1998;	98US-0100848P.	98US-0108779P.
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PR	23-SEP-1998;	98US-0101279P.	98US-0108806P.
PR	23-SEP-1998;	98US-0101471P.	98US-0108807P.
PR	23-SEP-1998;	98US-0101472P.	98US-0108867P.
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PR	23-SEP-1998;	98US-0101475P.	98US-0108848P.
PR	23-SEP-1998;	98US-0101476P.	98US-0108849P.
PR	23-SEP-1998;	98US-0101477P.	98US-0108850P.
PR	23-SEP-1998;	98US-0101478P.	98US-0108851P.
PR	24-SEP-1998;	98US-0101738P.	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	98US-0108858P.
PR	24-SEP-1998;	98US-0101915P.	98US-0108904P.
PR	24-SEP-1998;	98US-0101916P.	98US-0113236P.
PR	29-SEP-1998;	98US-0102207P.	98US-0114223P.
PR	29-SEP-1998;	98US-0102240P.	98US-0114223P.
PR	29-SEP-1998;	98US-0102240P.	98US-0114223P.
PR	29-SEP-1998;	98US-0102307P.	98US-0114223P.
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PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams FM, Wood WI;
XX
XX WPI; 2003-595293/55.
DR N-PSDB; ACD68242.
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XX
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2a-63;
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KW T-lymphocyte proliferation; endothelial cell apoptosis;
KW c-fos stimulation; pancreatic beta cell differentiation;
KW chondrocyte proliferation; glucose uptake; free fatty acid; FFA uptake;
KW tissue typing.
XX
XX Homo sapiens.
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XX 06-MAR-2003.
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XX 01-FEB-2002; 2002US-00066211.
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XX
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
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XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
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XX WPI; 2003-492259/46.
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XX N-PSDB; ACH04344.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating various cardiac insufficiency
XX disorders, bone and/or cartilage disorders such as sports injuries and
XX arthritis.

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AC ABO33460;
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KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine.
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OS Homo sapiens.
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XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX
XX WPI; 2003-585292/55.
XX N-PSDB; ACD67888.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 12; Fig 4; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I), having at least 80% sequence identity to a sequence
XX
XX Query Match 100.0%; Score 609; DB 7; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 2e-63;
XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MIVFGWAVFLASRLGQLLITLLEHIAHFLGTGGAATTMGNSICICRDDSGTDSVDTQ 60
Db 1 MIVFGWAVFLASRLGQLLITLLEHIAHFLGTGGAATTMGNSICICRDDSGTDSVDTQ 60
Qy 61 QQAENSAPVPTADTRSPQDPVPRPRGRGPHPRKKNQVDGLVLTAVIRTLVDK 117
Db 61 QQAENSAPVPTADTRSPQDPVPRPRGRGPHPRKKNQVDGLVLTAVIRTLVDK 117

RESULT 11
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ID AB019838 standard; protein; 117 AA.
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XX AC AB019838;
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XX DT 29-AUG-2003 (first entry)
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XX DE Human secreted/transmembrane protein PRO444.
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XX KW Human; PRO; secreted and transmembrane protein; gene therapy;
XX enterocolitis; gastrointestinal ulceration; skin disease; asthma;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; inflammatory disease; organ failure;
XX rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
XX cardiac injury; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair.
XX
XX OS Homo sapiens.
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XX PN US2003044902-A1.
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XX PD 06-MAR-2003.
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XX PF 01-FEB-2002; 2002US-00066193.
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XX 26-AUG-1997; 97US-0056974P.
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98US-0100607P.
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98US-0100609P.
98US-0100610P.
98US-0100611P.
98US-0100
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(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gao W, Gerber H, Grittisen ME, Goddard A;
 PI Godowski EJ, Gurney AL, Kljavin IJ, Mather JP, Napier WA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-492261/46.
 DR N-PSDB; ACD30202.

XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
 DR treating inflammatory diseases, organ failure, atherosclerosis, cardiac
 PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
 PT disease.

XX Claim 21; Fig 4; 154pp; English.

XX The invention relates to an isolated native sequence PRO polypeptide
 CC (secreted and transmembrane protein) having 80% sequence similarity to
 CC one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO
 CC extracellular domain (with or without a signal peptide) encoded by a
 CC nucleic acid 80% identical to one of 37 cDNA sequences, shown in the
 CC specification. Also included are vectors comprising the PRO nucleic
 CC acids, host cells comprising the vectors (used to produce the PRO
 CC proteins), a chimaeric molecule comprising the PRO polypeptide fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, linking a
 CC bioactive molecule to a cell expressing the PRO polypeptides and
 CC modulating at least one biological activity of a cell expressing the
 CC polypeptides. The PRO polypeptides and nucleic acids are useful in
 CC diagnosing or treating enterocolitis, gastrointestinal ulceration, skin
 CC diseases associated with abnormal keratinocyte differentiation, e.g.
 CC psoriasis or epithelial cancers such as squamous cell carcinoma,
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
 CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, AIDS, cancer, diabetic complications, or
 CC mutations in general. The polypeptides are also useful for wound repair
 CC and associated therapies concerned with re-growth of tissue. The
 CC nucleotide sequences may be used as hybridisation probes in chromosome
 CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
 CC acids are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in binding reaction, to
 CC generate transgenic animals or knockout animals, which in turn are useful
 CC in the development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides and
 CC nucleic acid molecules are also useful in gene therapy, and as molecular
 CC weight markers for protein electrophoresis purposes. The anti-PRO
 CC antibodies may be used in diagnostic assays for PRO, or for the affinity
 CC purification of PRO from recombinant cell culture or natural sources. The
 CC present sequence represents a PRO protein of the invention

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRSIGQGLLTLEEHIAFLGTGGAATMGNSICRDDSGTDSVDTQ 60
 Db 1 MIVFGWAVFLASRSIGQGLLTLEEHIAFLGTGGAATMGNSICRDDSGTDSVDTQ 60
 QY 61 QOAEASVPTATRSQPRDPVPRGRGPHPRKKONVGLVLTAVIRTLVDK 117
 Db 61 QOAEASVPTATRSQPRDPVPRGRGPHPRKKONVGLVLTAVIRTLVDK 117

RESULT 12

ADCI7875

ID ADCI7875 standard; protein; 117 AA.

XX ADCI7875;

XX

DT 19-DEC-2003 (first entry)
 XX Human PRO polypeptide #2.
 XX Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
 KW genetic disorder.
 XX Homo sapiens.
 XX US2003064925-A1.
 XX 03-APR-2003.
 XX 10-DEC-2001; 2001US-00013907.
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 03-SEP-1998; 98US-0099536P.
 PR 03-SEP-1998; 98US-0099596P.
 PR 03-SEP-1998; 98US-0099598P.
 PR 03-SEP-1998; 98US-0099602P.
 PR 03-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 13-SEP-1998; 98US-0100385P.
 PR 13-SEP-1998; 98US-0100390P.
 PR 13-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100948P.
 PR 18-SEP-1998; 98US-0100949P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 25-SEP-1998; 98US-0102207P.
 PR 25-SEP-1998; 98US-0102240P.
 PR 25-SEP-1998; 98US-0102307P.
 PR 25-SEP-1998; 98US-0102330P.
 PR 25-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.

XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX Homo sapiens.
 XX US2003105011-A1.
 XX 05-JUN-2003.
 XX 16-AUG-2002; 2002US-00223084.
 XX 15-SEP-2000; 2000US-0232887P.
 XX 20-JUN-2001; 2001WO-US019692.
 XX 09-JUL-2001; 2001WO-US021735.
 XX 20-FEB-2002; 2002US-00081056.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2003-810831/76.
 DR N-PSDB; ADD10294.
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX Claim 11; SEQ ID NO 6; 493pp; English.
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX Sequence 117 AA;
 XX Query Match 100.0%; Score 609; DB 7; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2e-63; Indels 0; Gaps 0;
 XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASSLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSDGSDSDVTQQ 60
 DB 1 MIVFGWAVFLASSLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSDGSDSDVTQQ 60
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 DB 61 QQAENSAPVTADTRSQPRDPVRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
 RESULT 14
 ADD11255
 ID ADD11255 standard; protein; 117 AA.
 XX AC ADD11255;
 XX

DT 01-JAN-2004 (first entry)
 XX Human secreted/transmembrane PRO polypeptide #3.
 DE human; secreted protein; transmembrane protein; cardiovascular disorder;
 XX endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX Homo sapiens.
 OS US2003105013-A1.
 XX 05-JUN-2003.
 XX 16-AUG-2002; 2002US-00223090.
 XX 20-JUN-2001; 2001WO-US019692.
 XX 09-JUL-2001; 2001WO-US021735.
 XX 20-FEB-2002; 2002US-00081056.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2003-801242/75.
 DR N-PSDB; ADD11254.
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, useful for treating a cardiovascular, endothelial, or
 PT angiogenic disorder in a mammal, such as cancer or age-related macular
 PT degeneration.
 XX Claim 11; SEQ ID NO 6; 493pp; English.
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX Sequence 117 AA;
 XX Query Match 100.0%; Score 609; DB 7; Length 117;
 XX Best Local Similarity 100.0%; Pred. No. 2e-63; Indels 0; Gaps 0;
 XX Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASSLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSDGSDSDVTQQ 60
 DB 1 MIVFGWAVFLASSLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSDGSDSDVTQQ 60
 QY 61 QQAENSAPVTADTRSQPRDPVRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
 DB 61 QQAENSAPVTADTRSQPRDPVRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
 RESULT 15
 ADD70521
 ID ADD70521 standard; protein; 117 AA.


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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WC-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WC-US020111.
PR 15-SEP-1999; 99WC-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WC-US028313.
PR 02-DEC-1999; 99WC-US028551.
PR 16-DEC-1999; 99WC-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US008520.
PR 01-MAR-2001; 2001WO-US008666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI,
XX
XX WPI; 2003-874602/81.
DR DR
DR N-PSDB; ADD70520.
XX
XX
XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Claim 12; SEQ ID NO 6; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;
OY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGTTDSVDTQQ 60
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGTTDSVDTQQ 60
OY 61 QQAENSAVPTADTRSPRPGRGPHPRKKQNVGVLDTLAVIRTLVDX 117
Db 61 QQAENSAVPTADTRSPRPGRGPHPRKKQNVGVLDTLAVIRTLVDX 117

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